









SQ Sequence 96 AA;

Query Match similarity 94.0%; score 487; DB 20; length 96;  
Best Local Similarity 95.8%; Pred. No. 5, 8e-53;  
Matches 92; Conservative 0; Mismatches 4; Indices 0; Gaps 0;

QY 1 MEWAHEPDPPEKPNWENLLEELKEAHPFPRKWLHSLGQDVEVYGVWGWAEAL 60  
DB 1 IRLQQQLEIHRIGRSRIGLQGQRPWNASKS 66

QY 61 IRLQQQLEIHRIGRSRIGLQGQRPWNASKS 66  
DB 61 IRLQQQLEIHRIGRSRIGLQGQRPWNASKS 96

RESULT 9  
AAW9823  
ID AAW9823 standard; protein: 96 AA.

XX AAW9823;  
KW cell proliferation, disease;  
PS Human immunodeficiency virus  
XX HIV 1.68 protein sequence.  
PN WO909412-A1.  
XX  
PT 25-FEB-1999.  
PF 14-AUG-1998; 98WO-US16890  
PK 14-AUG-1997; 97US-0055754.  
XX (WYETH) UNIV PENNSYLVANIA.  
PT AYER, V.; KICHLER, DIMONIS T.; MATHILAKAM S.; PATEL M.;  
PN Weiner, DB;  
XX WPI: 1999-181154/15.

XX Example: Fig 1B; 64PP; English.

PT Conjugate composition comprising HIV 1 Vpr protein fragment used  
to inhibit cell proliferation, and treating hyperproliferative  
diseases;  
XX Example: Fig 1B; 64PP; English.

CC The present invention describes a conjugate composition comprising a  
CC fragment of HIV-1 or non-HIV-1 Vpr protein conjugated to a therapeutic  
CC compound. The conjugate can be used in a method for inhibiting cell  
CC proliferation. It can also be used for treating an individual who has a  
CC hyperproliferative disease. The HIV-1 Vpr or non-HIV-1 Vpr protein  
CC fragments can be used for identifying compounds that inhibit Vpr protein  
CC binding to the p6 domain of p55 or to p6 protein. The present sequence  
CC represents an HIV protein sequence.

XX Sequence 96 AA;

Query Match similarity 94.0%; score 487; DB 20; length 96;  
Best Local Similarity 95.8%; Pred. No. 5, 8e-53;  
Matches 92; Conservative 1; Mismatches 4; Indices 0; Gaps 0;

QY 1 MEWAHEPDPPEKPNWENLLEELKEAHPFPRKWLHSLGQDVEVYGVWGWAEAL 60  
DB 1 IRLQQQLEIHRIGRSRIGLQGQRPWNASKS 66

QY 61 IRLQQQLEIHRIGRSRIGLQGQRPWNASKS 66  
DB 61 IRLQQQLEIHRIGRSRIGLQGQRPWNASKS 96

RESULT 10  
AAW9825  
ID AAW9825 standard; protein: 96 AA.

XX AAW9825;  
AC AAW9825;  
XX  
PT 08-JUN-1999 (first entry)  
XX HIV H71V protein sequence.  
XX HIV: Vpr; human immunodeficiency virus; hyperproliferative disease;  
KW cell proliferation.

XX Human immunodeficiency virus.  
XX WO909412-A1.  
PT 25-FEB-1999.  
PF 14-AUG-1998; 98WO-US16890.  
PK 14-AUG-1997; 97US-0055754.  
XX (WYFL-) UNIV PENNSYLVANIA.  
PT AYER, V.; KICHLER, DIMONIS T.; MATHILAKAM S.; PATEL M.;  
PN Weiner, DB;  
XX WPI: 1999-181154/15.

XX Example: Fig 1B; 64PP; English.

PT Conjugate composition comprising HIV 1 Vpr protein fragment used  
to inhibit cell proliferation, and treating hyperproliferative  
diseases;  
XX Example: Fig 1B; 64PP; English.

CC The present invention describes a conjugate composition comprising a  
CC fragment of HIV-1 or non-HIV-1 Vpr protein conjugated to a therapeutic  
CC compound. The conjugate can be used in a method for inhibiting cell  
CC proliferation. It can also be used for treating an individual who has a  
CC hyperproliferative disease. The HIV-1 Vpr or non-HIV-1 Vpr protein  
CC fragments can be used for identifying compounds that inhibit Vpr protein  
CC binding to the p6 domain of p55 or to p6 protein. The present sequence  
CC represents an HIV protein sequence.

XX Sequence 96 AA;

Query Match similarity 94.0%; score 487; DB 20; length 96;  
Best Local Similarity 95.8%; Pred. No. 5, 8e-53;  
Matches 92; Conservative 1; Mismatches 4; Indices 0; Gaps 0;

QY 1 MEWAHEPDPPEKPNWENLLEELKEAHPFPRKWLHSLGQDVEVYGVWGWAEAL 60  
DB 1 IRLQQQLEIHRIGRSRIGLQGQRPWNASKS 66

QY 61 IRLQQQLEIHRIGRSRIGLQGQRPWNASKS 66  
DB 61 IRLQQQLEIHRIGRSRIGLQGQRPWNASKS 96





4. Implementing the required tasks. The implementation of the required tasks is a process of identifying the required tasks and then carrying them out.

THE JOURNAL OF CLIMATE

Page  
1

GenCore version 4.5  
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(with front alignments) + latencies

Sect. 1. Introduction

Searched: 2023-02-09 06:45, 221847457 residues

Total number of hits satisfying selection criteria: 1125

Maxima 100-103 Sec 1 Ref ID: 2000000000

Maximum market value 100%  
Listed first 45 summaries

Database : Pending\_Patents\_AA\_Main;\*

and, if required, to submit to the Board of Education of the city or town in which the school is located, a copy of the proposed contract.

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THE JOURNAL OF CLIMATE

Score greater than or equal to the score of the result being printed and is defined by analysis of the total score distribution.

SUMMARIES

No.	Score	Quarter	Match	Length	LB	ID	Doorscript
1	47-0	90-7	96	6	18-0-0-5-24	6-64-1	Scorpion
2	47-0	90-7	96	18	18-0-0-9-4-54	1-16-1	Scorpion
3	47-0	90-7	96	18	0-3-3-4-1-54	1-16-1	Scorpion
4	46-1	89-0	96	11	18-0-8-7-0-4-0-0-67	1-16-1	Scorpion
5	46-1	89-0	96	17	18-0-9-7-0-9-5-7-1-9	1-16-1	Scorpion
6	46-1	89-0	96	21	18-0-9-7-0-9-6-1-19	1-16-1	Scorpion
7	32-2	7-7	103	18	18-0-9-4-2-2-9-1-2-1-18	1-16-1	Scorpion
8	36-7	7-0-8	100	18	18-0-9-4-2-2-9-7-8-1-15	1-16-1	Scorpion
9	46-5	7-0-6	100	18	18-0-9-4-2-2-9-7-8-1-15	1-16-1	Scorpion
10	36-1	6-9-7	72	9	18-0-8-5-2-4-6-9-4	1-16-1	Scorpion



1.0  
6.1 IRL1QQLIPIRGPGRKRSRQVYRURKARNASRS 96  
US 09/700,408 67

RESULT 4  
S-PROTEIN 6.5 Application US/09700409

GENERAL INFORMATION:

APPLICANT: Asali, Rashed A.

APPENDANT: Arunachari, Chinnath

TITLE OF INVENTION: VPR AND VTX PROTEINS OF HIV

NUMBER OF SEQUENCES: 74

CORRESPONDENCE ADDRESS:

ASALI, RASHED A., P.O. BOX 101, 1111 HUMAN ANG STREETS, FRED,

STREET: 400 SEVENTH STREET, N.W.,  
CITY: WASHINGTON

STATE: D.C.  
ZIP: 20004

COMPUTER PROGRAM NAME:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US 09/700,408

FILING DATE: 25 NOV 1996

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

FILING DATE: 25 MAR 1994

PREV. APPLICATION DATA:

APPLICATION NUMBER: AU 959902

FILING DATE: 14 SEP 1995

ATTORNEY/AGENT: THT, F.M.A.; M

NAME: Holman, John C.

REGISTRATION NUMBER: 22,769

REFERENCE NUMBER: 99434746388002

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-391-5350

TELEFAX: 202-391-5350

INFORMATION FOR SEQ ID NO: 67:

SEQUENCE CHARACTERISTICS:

LENGTH: 96 amino acids

TYPE: amino acid

STRANGLINESS:

UNPOLYMERIZABLE:

MIXTURE TYPE: peptide

OS-09-700,408-7

Query Match: 84% Score: 461; DB: 11; Length: 96;

Best local similarity: 35.5%; Fred: 0.0; Gaps: 0;

Matches: 84; Conservative: 7; Mismatches: 5; Indels: 0; Gaps: 0.

OY 1 MEQAPEDQPOREPNWDTLLEELKEAVRHPRIWHISLGQHIVTYGVWGVAF 60

1 MEQAPEDQPOREPNWDTLLEELKEAVRHPRIWHISLGQHIVTYGVWGVAF 60

QF 6.1 IRIL2QQLIPIRGPGRKRSRQVYRURKARNASRS 96

6.1 IRIL2QQLIPIRGPGRKRSRQVYRURKARNASRS 96

RESULT 5  
US-09-700,408-7

Sequence 19, Application US, sequence 2

GENERAL INFORMATION:

APPENDANT: Heidrich, Peter; Institut für Biologie, Institut für Biologische Technik, Berlin

FILE REFERENCE: EP04381

CURRENT APPLICATION NUMBER: DE 09/700,408 572

CURRENT FILING DATE: 1999-05-11  
EARLIER APPLICATION NUMBER: DE 1998-5-6 463  
EARLIER FILING DATE: 1998-11-25

NUMBER OF SEQ ID NO: 24

SEQ ID NO: 19

LENGTH: 96

TYPE: PRT

ORGANISM: Human immunodeficiency virus type 1

FEATURE: vpr protein

OTHER INFORMATION: vpr protein

OS-09-718-096-19

Query Match: 89.0% Score: 465; DB: 17; length: 96;

Best Local Similarity: 87.5%; Prod.: No. 9.5<4.9; Matches: 84; Conservative: 7; Mismatches: 5; Indels: 0; Gaps: 0;

OY 1 MEQAPEDQPOREPNWDTLLEELKEAVRHPRIWHISLGQHIVTYGVWGVAF 60

1 MEQAPEDQPOREPNWDTLLEELKEAVRHPRIWHISLGQHIVTYGVWGVAF 60

QF 6.1 IRIL2QQLIPIRGPGRKRSRQVYRURKARNASRS 96

6.1 IRIL2QQLIPIRGPGRKRSRQVYRURKARNASRS 96

RESULT 6  
US-09-718-096-19

Query Match: 89.0% Score: 465; DB: 17; length: 96;

Best Local Similarity: 87.5%; Prod.: No. 9.5<4.9; Matches: 84; Conservative: 7; Mismatches: 5; Indels: 0; Gaps: 0;

OY 1 MEQAPEDQPOREPNWDTLLEELKEAVRHPRIWHISLGQHIVTYGVWGVAF 60

1 MEQAPEDQPOREPNWDTLLEELKEAVRHPRIWHISLGQHIVTYGVWGVAF 60

QF 6.1 IRIL2QQLIPIRGPGRKRSRQVYRURKARNASRS 96

6.1 IRIL2QQLIPIRGPGRKRSRQVYRURKARNASRS 96

RESULT 7  
US-09-717A-119

Query Match: 89.0% Score: 462; DB: 17; length: 96;

Best Local Similarity: 87.5%; Prod.: No. 9.5<4.9; Matches: 84; Conservative: 7; Mismatches: 5; Indels: 0; Gaps: 0;

OY 1 MEQAPEDQPOREPNWDTLLEELKEAVRHPRIWHISLGQHIVTYGVWGVAF 60

1 MEQAPEDQPOREPNWDTLLEELKEAVRHPRIWHISLGQHIVTYGVWGVAF 60

QF 6.1 IRIL2QQLIPIRGPGRKRSRQVYRURKARNASRS 96

6.1 IRIL2QQLIPIRGPGRKRSRQVYRURKARNASRS 96

RESULT 8  
US-09-717A-201A

Query Match: 89.0% Score: 462; DB: 17; length: 96;

Best Local Similarity: 87.5%; Prod.: No. 9.5<4.9; Matches: 84; Conservative: 7; Mismatches: 5; Indels: 0; Gaps: 0;

OY 1 MEQAPEDQPOREPNWDTLLEELKEAVRHPRIWHISLGQHIVTYGVWGVAF 60

1 MEQAPEDQPOREPNWDTLLEELKEAVRHPRIWHISLGQHIVTYGVWGVAF 60

QF 6.1 IRIL2QQLIPIRGPGRKRSRQVYRURKARNASRS 96

6.1 IRIL2QQLIPIRGPGRKRSRQVYRURKARNASRS 96

RESULT 9  
US-09-717A-201A

Query Match: 89.0% Score: 462; DB: 17; length: 96;

Best Local Similarity: 87.5%; Prod.: No. 9.5<4.9; Matches: 84; Conservative: 7; Mismatches: 5; Indels: 0; Gaps: 0;

OY 1 MEQAPEDQPOREPNWDTLLEELKEAVRHPRIWHISLGQHIVTYGVWGVAF 60

1 MEQAPEDQPOREPNWDTLLEELKEAVRHPRIWHISLGQHIVTYGVWGVAF 60

QF 6.1 IRIL2QQLIPIRGPGRKRSRQVYRURKARNASRS 96

6.1 IRIL2QQLIPIRGPGRKRSRQVYRURKARNASRS 96

RESULT 10  
US-09-717A-201A

Query Match: 89.0% Score: 462; DB: 17; length: 96;

Best Local Similarity: 87.5%; Prod.: No. 9.5<4.9; Matches: 84; Conservative: 7; Mismatches: 5; Indels: 0; Gaps: 0;

OY 1 MEQAPEDQPOREPNWDTLLEELKEAVRHPRIWHISLGQHIVTYGVWGVAF 60

1 MEQAPEDQPOREPNWDTLLEELKEAVRHPRIWHISLGQHIVTYGVWGVAF 60

QF 6.1 IRIL2QQLIPIRGPGRKRSRQVYRURKARNASRS 96

6.1 IRIL2QQLIPIRGPGRKRSRQVYRURKARNASRS 96





118 - 700 - 408 - 68

PROT. REC'D. NO. 117  
RECORDED BY: JONES, GENE  
RECORDED AT: BIRMINGHAM, ALABAMA  
RECORDED ON: 04-08-2000  
PAGE: 1 OF 4  
1910-19 BILLING DATE: 1998-07-06  
NUMBER OF SITES: 1  
NUMBER OF RECORDS: 8  
FILE NO.: 117  
NAME: GENE  
TYPE: FAX  
RECORDED BY: GENE JONES  
RECORDED ON: 04-08-1998  
PAGE: 1 OF 4

Category	Match	Score	Ques	DB	Topic
Forest	Forest	100%	Q25	DB-185	Forests
Mountain	Mountain	100%	Q26	DB-186	Mountains
Marches	Marches	100%	Q27	DB-187	Marches
Coast	Coast	100%	Q28	DB-188	Coast
Plain	Plain	100%	Q29	DB-189	Plains
Highland	Highland	100%	Q30	DB-190	Highlands
Steppe	Steppe	100%	Q31	DB-191	Steppe
Desert	Desert	100%	Q32	DB-192	Deserts
Woods	Woods	100%	Q33	DB-193	Woods
Glacier	Glacier	100%	Q34	DB-194	Glaciers
Marsh	Marsh	100%	Q35	DB-195	Marshes
Cliff	Cliff	100%	Q36	DB-196	Cliffs
Valley	Valley	100%	Q37	DB-197	Valleys
Island	Island	100%	Q38	DB-198	Islands
Peak	Peak	100%	Q39	DB-199	Peaks
Clay	Clay	100%	Q40	DB-200	Clay
Sand	Sand	100%	Q41	DB-201	Sand
Rock	Rock	100%	Q42	DB-202	Rock
Gravel	Gravel	100%	Q43	DB-203	Gravel
Soil	Soil	100%	Q44	DB-204	Soil
Ground	Ground	100%	Q45	DB-205	Ground
Groundwater	Groundwater	100%	Q46	DB-206	Groundwater
Minerals	Minerals	100%	Q47	DB-207	Minerals
Vegetation	Vegetation	100%	Q48	DB-208	Vegetation
Flora	Flora	100%	Q49	DB-209	Flora
Fauna	Fauna	100%	Q50	DB-210	Fauna

RESULT  
US-09-200-551-49  
SEQUENCE NO.: APPLICATION US/09/200551  
NAME: J. M. KELLY, JR.  
APPLICANT: Haskin Research  
ADDRESS: 1000 Park Avenue  
APPLICATION: BART & PRESTON  
TITLE OF INVENTION: A METHOD FOR DETERMINING THE PRESENCE OF A CERTAIN IMMUNODEFICIENCY VIRUS FROM A RABBIT TISSUE SAMPLE  
TITLE REFERENCE: 3,632,400  
CURRENT APPLICATION NUMBER: 3,632,400, 5,511  
NUMBER OF SEQ ID NOS.: 56  
SOFTWARE: PolyEdit Ver. 2.0  
LENGTH: 100  
TYPE: PCT  
ORGANISM: Simian immunodeficiency virus  
US-09-200-551-49

Sequence 56, APPI  
Sequence 56, APPI  
Sequence 4, APPI  
Sequence 10, APPI  
Sequence 6, APPI  
Sequence 3, APPI  
Sequence 14, APPI  
Sequence 23, APPI  
Sequence 30, APPI  
Sequence 2, APPI  
Sequence 7, APPI  
Sequence 25, APPI  
Sequence 36, APPI  
Sequence 4, APPI  
Sequence 36, APPI  
Sequence 4, APPI  
Sequence 3, APPI  
Sequence 7, APPI

Patent No. 6,042,842  
 INVENTOR: KOPROWSKI, Hilary  
 APPLICANT: KOPROWSKI, Hilary  
 ADDRESS: 1000 Chestnut Street, Philadelphia, PA  
 APPLICANT: Bokroska, Anna  
 TITLE OF INVENTION: Polypeptides based with Plant Virus  
 FIELD OF INVENTION: Coat Proteins  
 NUMBER OF STAPLES/EST.: 16  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Alan B. Etting & Associates  
 STREET: 1525 Locust Street, 15th Floor  
 CITY: Philadelphia  
 STATE: Pennsylvania  
 COMPANY: USA  
 ZIP: 19102  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: +COPY DISK  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: MS-DOS  
 SOFTWARE: Corel Wordperfect  
 COUNTRY APPLICATION MADE:  
 APPLICANT REMARK: 09/08/97, 7/4/86  
 FILING DATE: 28-Aug-1996  
 CLASSIFICATION:  
 ATTORNEY/AGENT/INVENTOR:  
 NAME: Fried, Allan H.  
 REGISTRATION NUMBER: 34,253  
 REFERENCE/PIRGT NUMBER: 119-007  
 TELEPHONE: (215) 742-7090  
 TELEFAX: (215) 742-7090  
 INFORMATION FOR SWID NO: 15:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 96 amino acids  
 TYPE: amino acid  
 DIVERSITY: Linear  
 HYBRIDOMA: N  
 US 08-704-856C-15

RESULT 4  
 US-099 124 900-5  
 Sequence 5: Application, US/099124900  
 Patent No. 6,264,842  
 GENERAL INFORMATION:  
 APPLICANT: KATZINGER, Hermann  
 APPLICANT: HUCHLER, Andrea  
 APPLICANT: ERNST, Wolfram  
 APPLICANT: BALAINI, Claudia  
 APPLICANT: HIRSCH, Martin  
 APPLICANT: HERZ, Alexander  
 APPLICANT: PFEIFER, Reiner  
 APPLICANT: SCHMID, Christine  
 APPLICANT: KLEIN, Albrecht  
 APPLICANT: KLEIN, Albrecht  
 APPLICANT: MOSER, Thomas  
 APPLICANT: MOSER, Thomas  
 TITLE OF INVENTION: HIV-Vecodex  
 FILER REFERENCE: 1049-112P

CURRENT FILING DATE: 1998-07-30  
 PRIORITY DATE: N/A  
 PRIORITY FILING DATE: 1995-04-19  
 NUMBER OF SEQ ID NOS: 11  
 SOFTWARE: PatentIn version 3.0  
 SEQ ID NO: 5  
 LENGTH: 78  
 TYPE: PCT  
 ORGANISM: Human immunodeficiency virus type 1  
 US-09-124-900-5

best local similarity: 91.7%; pred. No. 1, 9e-39;  
 matches: 67, consistency: 2, mismatch: 4; index: 0;  
 QRY I MEAQAFDQPOPEPHNWLLEIFLKEKNAFVAVHPRWHLGQHWTYKIDNGVEAEL 60  
 DB I MEAQAFDQPOPEPHNWLLEIFLKEKNAFVAVHPRWHLGQHWTYKIDNGVEAEL 60  
 QRY 61 RILQQLIPHF 72  
 DB 61 RILQQLIPHF 72  
 QRY 61 RILQQLIPHF 72  
 DB 61 RILQQLIPHF 72

RESULT 5  
 US-08-401-445-4  
 Sequence 4, Application US-08-401-445-4  
 PCT/US97/06116  
 GENERAL INFORMATION:  
 APPLICANT: CABIN, ERIC A.  
 APPLICANT: BERERON, Dominique  
 APPLICANT: CHOURONE, Florent  
 INVENTOR: YAO, XIAO-JIANG  
 TITLE OF INVENTION: BASED ON HIV-1 VIR FUSION MOLECULES  
 NUMBER OF SEQUENCES: 5  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEES: KLAUBER & JACKSON  
 SUBJECT: Confidential Plaintiff, 411 Hackensack Avenue  
 CITY: Hackensack  
 STATE: NJ  
 COUNTRY: U.S.A.  
 ZIP: 07601  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: FLOPPY DISK  
 COMPUTER: IBM PC compatible  
 ATTACHING SYSTEM: Floppy disk  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: 26,742  
 FILING DATE: September 7, 1995  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: JACKSON, David A.  
 REGISTRATION NUMBER: 26,742  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 201-487-5800  
 TELEFAX: 201-344-1684  
 TELEX: 133721  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 72 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 HYPOTHETICAL: NO  
 QRY 68 524 69A 4

RESULT 6  
 US-08-524-69A-4  
 Sequence 4, Application US-08-524-69A-4  
 PCT/US97/06101  
 GENERAL INFORMATION:  
 APPLICANT: CABIN, ERIC A.  
 APPLICANT: BERERON, Dominique  
 APPLICANT: CHOURONE, Florent  
 APPLICANT: YAO, XIAO-JIANG  
 APPLICANT: PIGNAC-KOBINGER, Gaby  
 TITLE OF INVENTION: PROTEIN TARGETING INTO HIV VIRIONS BASED  
 NUMBER OF SEQUENCES: 5  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEES: KLAUBER & JACKSON  
 SUBJECT: Confidential Plaintiff, 411 Hackensack Avenue  
 CITY: Hackensack  
 STATE: NJ  
 COUNTRY: U.S.A.  
 ZIP: 07601  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: FLOPPY DISK  
 COMPUTER: IBM PC compatible  
 ATTACHING SYSTEM: Floppy disk  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: 26,742  
 FILING DATE: September 7, 1995  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: JACKSON, David A.  
 REGISTRATION NUMBER: 26,742  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 201-487-5800  
 TELEFAX: 201-344-1684  
 TELEX: 133721  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 72 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 HYPOTHETICAL: NO  
 QRY 68 524 69A 4

RESULT 9  
US-08-524 694A-2  
; Sequence 2, Application 05/085,246/94  
; Patent No. 6,043,081

THE JOURNAL OF CLIMATE VOL. 19, NO. 1, JANUARY 2006

UNIVERSITÉ INFORMATIQUE  
ALPHONSE CHEN, Eric A.  
ALPHONSE BELIBAH, Dominique  
ALPHONSE CHEVREAU, Florent  
ALPHONSE YAN, Xiaotian

THE JOURNAL OF CLIMATE

APPLICANT: PIGNATI, KERBLINGER, Gary  
TITLE OF INVENTION: PROTEIN TARGETING INTO HIV  
NUMBER OF INVENTORS: 5  
NUMBER OF SPECIMENS: 5

卷之三

OUR  
CIRKUS'S RESIDENCE ADDRESS:  
ADDRESS: KATTEBEK & JACKSON  
STREET: Continental Plaza, 411 MARKET, SAN FRANCISCO.

GENERAL INFORMATION:  
APPELLANT: JOHN ERIC A.  
APPELLEE: BREVILLE DOMINIQUE

STATE: N.J.  
COUNTRY: U.S.A.  
ZIP: 07601

APRIL 10, 1911. - SAN FRANCISCO, CALIFORNIA. - PATENT AND TRADE MARK OFFICE.

**MEILLEUR TYPE** : floppy disk COMPATIBLE IBM PC COMPATIBLE

NUNHOMPS P. S. G. H. T. C.  
N. A. B. E. R. N. H. S. H. S. S.  
A. M. O. R. K. E. R. K. E. R. K. E. R.

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: 102,082,624, 6-94A  
FILING DATE: September 7, 1995

ATTORNEY/AGENCY INFORMATION:  
NAME: JACKSON, David A.  
REGISTRATION NUMBER: 26-742

W. M. L. K. READING ROOM,  
MICHIGAN LIBRARY, BLDG., ANN ARBOR,  
MICHIGAN.

TELEPHONE: 201-487-5810  
TELEFAX: 201-343-1684  
TELEX: 13352

WILSON: I want to see where it is. VERSUS  
WILSON: KNEW WHAT IT WAS  
AFTER TALKING WITH SAWYER.

SEQUENCE CHARACTERISTICS:  
LENGTH: 105 amino acids  
TYPE: amino acid

AN ASSOCIATION OF  
PRACTITIONERS IN  
NATURAL MEDICINE.

**TOPOLOGY:** Linear  
**MATERIAL TYPE:** protein  
**ENVIRONMENT:** Soil

DS-08-524-694A 2

RESULT: 11  
US-09-485-490-9  
Sequence: 9; Application US-09-485-490  
Patent No.: 6,258,308  
GENERAL INFORMATION:  
APPLICANT: Kraus, Gunter  
APPLICANT: Wong-Saal, Flossie  
APPLICANT: Talbott, Randy  
APPLICANT: Poeschla, Eric  
TITLE OF INVENTION: Isolation of No. 588981 HIV 2 Proviruses  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
RECEPTEE: Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIA TYPE: 3½" Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: BioEdit Version 5.0  
CURRENT APPLICATION DATA:  
Applicant: Kraus, Gunter  
Filing Date: Nov 5, 1998  
Classification: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/2001,441  
FILING DATE: 26-JUL-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Garrett-Walkowski, Ragenta  
REGISTRATION NUMBER: 37,340  
PEPERMUTATION NUMBER: 32007  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0400  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 105 amino acids  
TYPE: protein  
STRANDEDNESS:  
TOPOLOGY: Linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..105  
OTHER INFORMATION: Note - "prf" protein encoded by HTV 2K®  
US-08-659-251-9

Query Match Similarity: 36.18%; Score: 187; DB: 27; Length: 105;  
Best Local Similarity: 46.3%; Freq. No.: 8; Ic: 17; Index: 2; Caps: 2;  
Matches: 38; Conserving: 16; Mismatches: 26; Indexes: 2; Caps: 2;  
Matches: 38; Conserving: 16; Mismatches: 26; Indexes: 2; Caps: 2;

QY 61 IRDQDQIPIHGRGSRIG 82  
DB 66 INVQLRALKVHLRAGCKRIG 87  
ID 66 INVQLRALKVHLRAGCKRIG 87

RESULT: 12  
US-09-485-490-9  
PCP-US96-111445-9  
Sequence: 9; Application PCP-US96-111445  
GENERAL INFORMATION:  
APPLICANT: The Regents of the University of California  
TITLE OF INVENTION: Isolation of Novel HIV-2 Proviruses  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
RECEPTEE: Robins, Barristers Carson  
STREET: 201 N. Figueroa Street, 5th floor  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90012-2628  
COMPUTER READABLE FORM:  
MEDIA TYPE: Floppy disk

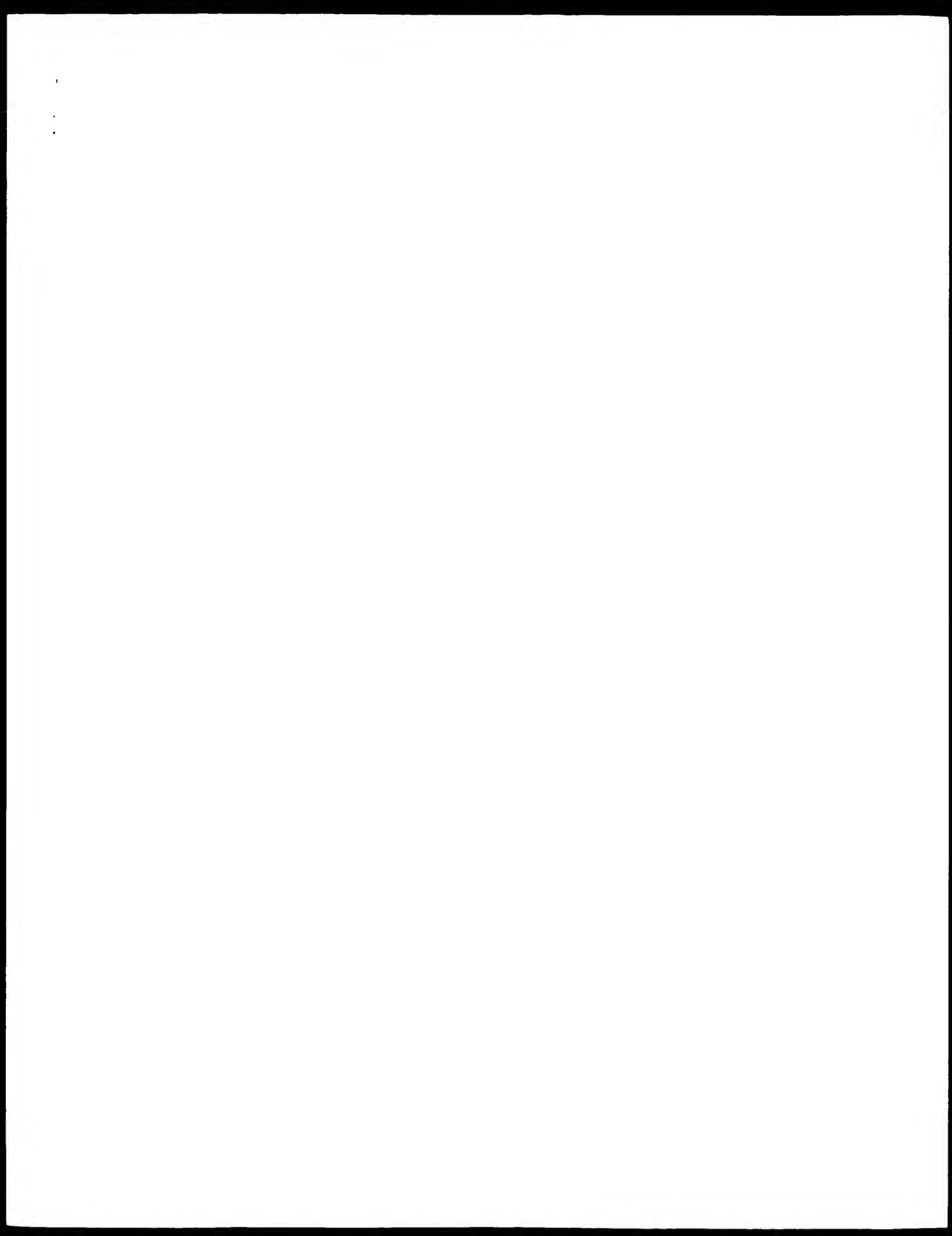


Db : 83 CKKJGK 88  
 RESULT : 15  
 PCF-US93-04301-2  
 Sequence 2, Application PC/US9304301  
 GENERAL INFORMATION:  
 APPLICANT: Mylon R. Essex et al.  
 TITLE OF INVENTOR: AIDS Therapeutics Based on HIV-2  
 TITLE OF INVENTION: Vpx Peptides  
 NUMBER OF SEQUENCES: 8  
 CORRESPONDENT ADDRESS:  
 ADDRESSE: Fish & Richardson  
 STREET: 225 Franklin Street  
 CITY: Boston  
 STATE: MA  
 COUNTRY: U.S.A.  
 ZIP: 02110-2804  
 COMPUTER READABLE FORM:  
 COMPUTER TYPE: IBM PC compatible  
 OPERATING SYSTEM: PC DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: 08/115,554 301  
 FILING DATE: 19930507  
 CLASSIFICATION:  
 ATTORNEY/REMITTING: RE  
 NAME: Freeman, John W.  
 REGISTRATION NUMBER: 29,066  
 RIFLEMAN NUMBER: 30017001  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 617/542-5070  
 TELEFAX: 617/542-8906  
 INFORMATION FROM SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 112  
 TYPE: AMINO ACID  
 STRANDEDNESS:  
 TOPOLOGY: linear  
 SEQ ID US93-04301-2

Query Match Similarity: 16.38; Score: 84.53; DB %: Length: 112;  
 Rest, Local: 27.38; Prod. No.: 0.3014; Index: 5%; Gaps: 1;  
 Matches: 18; Conservative: 15; Mismatches: 28;

QY 17 DWTEELLEKNEAVRHEPRWHSQHUYEGIWWGVWALK----LICQJLPH 71  
 DB 23 FWRKIVVTRKAVVHLRFLFQWKRSSWYWHRBESSESYIKYKLSLWKALFVH 82  
 QY 72 FRIGCR 77  
 DB 83 CKKJGK 88

Search completed: october 3, 2001, 13:21:17  
 Job time: 20 sec



GenCore version 4.5  
Copyright (c) 1994 - 2000 GenCore LLC.

Q: protein - protein search, using SW model  
Format: october 3, 2001, 13:29:57 - 30.034 + rms 1.1, v. 2.00, 0d.  
Database: 489,148 million cell updates/sec  
Title: US-09-485-421-1  
Fitter score: 518  
Sequence: 1 MEAQADQDQDPYPPNWTI  
Starting table: BLASTME2  
GapOp: 10.0 , GapExt: 0.5

Searched:

219241 seqs, 76174552 residues

Minimum DB seq length: 0

Maximum DB seq length: 200000

Post-processing: Minimum Match 0.9

Maximum Match 1.00%

Listing first 45 Submatches

Database :  
1: PIR:f8; \*  
2: PIR:2; \*  
3: PIR:3; \*  
4: PIR:4; \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARY

Result No.	Score	Query	Description
1	45.9	804 6	vpr
2	45.4	87 6	vpr
3	44.8	93 6	vpr
4	44.5	85 9	vpr
5	44.5	35 2	vpr
6	40.2	96 1	vpr
7	24.8	47 9	vpr
8	24.8	47 9	vpr
9	24.7	47 7	vpr
10	24.5	47 4	vpr
11	24.3	47 0	vpr
12	24.4	45 6	vpr
13	22.4	43 2	vpr
14	22.5	42 8	vpr
15	21.5	41 4	vpr
16	21.9	41 5	vpr
17	21.9	40 5	vpr
18	21.9	39 4	vpr
19	15.3	29 5	vpr
20	19.1	19 1	vpr
21	97.5	18 8	vpr
22	93.5	18 1	vpr
23	92.5	17 6	vpr
24	90.5	17 5	vpr
25	84.5	16 3	vpr
26	84.5	16 3	vpr
27	84.5	11 2	vpr
28	83.4	11 2	vpr
29	83.4	11 2	vpr
30	79.5	11 2	vpr

RESULT 1  
Query Match 89.6%, Score 45.9; DR 27; Length 96;  
Best Local Similarity 87.5%; Prog. No.: 2; Gaps: 0;

Matches 84; Consistency: 7, Mismatches: 5; Indels: 0; Gaps: 0;  
P5: 1 MEAQADQDQDPYPPNWTI  
C: Species: human immunodeficiency virus type 1, HIV-1  
G: Accession: T09444  
P: Pari, S.; Vinters, H.V.; Akashi, T.; O'Bryan, W.A.; Chou, I.S.; Kyunggi, Y.; Kazar  
Submitted to the EMBL Data Library, July 1996  
A: Reference number: Z16673  
A: Accession: T09444  
A: Status: Preliminary; translated from SWISSPROT/PIRDB  
A: Molecule type: DNA  
A: Residues: 1-96; SPAN: A  
A: Cross-references: EMBL:U66632; MID:91465777; PID:91465784  
C: Genetics: vpr  
C: Sequencefamily: AIDS vpr protein

vpr protein - simi  
orf-X protein - simi  
vpr protein - huma  
vpr protein - huma  
vpr protein - huma  
vpr protein - huma  
probable membrane  
vpx protein - huma  
vpx protein - huma  
vpx protein - huma  
hypothetical prote  
beta glucosidase  
vpr protein - human  
hypothetical prote  
aaas protein - Escherichia coli  
pathogenesis-related  
1-phosphatidylinositol

#### ALIGNMENTS

219241 seqs, 76174552 residues

Total number of hits satisfying above parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 200000

Post-processing: Minimum Match 0.9

Maximum Match 1.00%

Listing first 45 Submatches

Database :  
1: PIR:f8; \*  
2: PIR:2; \*  
3: PIR:3; \*  
4: PIR:4; \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARY

Result No.	Score	Query	Description
1	45.9	804 6	vpr
2	45.4	87 6	vpr
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8	24.8	47 9	vpr
9	24.7	47 7	vpr
10	24.5	47 4	vpr
11	24.3	47 0	vpr
12	24.4	45 6	vpr
13	22.4	43 2	vpr
14	22.5	42 8	vpr
15	21.5	41 4	vpr
16	21.9	41 5	vpr
17	21.9	40 5	vpr
18	21.9	39 4	vpr
19	15.3	29 5	vpr
20	19.1	19 1	vpr
21	97.5	18 8	vpr
22	93.5	18 1	vpr
23	92.5	17 6	vpr
24	90.5	17 5	vpr
25	84.5	16 3	vpr
26	84.5	16 3	vpr
27	84.5	11 2	vpr
28	83.4	11 2	vpr
29	83.4	11 2	vpr
30	79.5	11 2	vpr

RESULT 2  
Query Match 89.6%, Score 45.9; DR 27; Length 96;  
Best Local Similarity 87.5%; Prog. No.: 2; Gaps: 0;

Matches 84; Consistency: 7, Mismatches: 5; Indels: 0; Gaps: 0;  
P5: 1 MEAQADQDQDPYPPNWTI  
C: Species: human immunodeficiency virus type 1, HIV-1  
G: Accession: T09444  
P: Pari, S.; Vinters, H.V.; Akashi, T.; O'Bryan, W.A.; Chou, I.S.; Kyunggi, Y.; Kazar  
Submitted to the EMBL Data Library, July 1996  
A: Reference number: Z16673  
A: Accession: T09444  
A: Molecule type: DNA  
A: Residues: 1-96; SPAN: A  
A: Cross-references: EMBL:U66632; MID:91465777; PID:91465784  
C: Genetics: vpr

vpr protein - simi  
orf-X protein - simi  
vpx protein - huma  
vpx protein - huma  
vpx protein - huma  
vpx protein - huma  
probable membrane  
vpx protein - huma  
vpx protein - huma  
vpx protein - huma  
hypothetical prote  
beta glucosidase  
vpr protein - human  
hypothetical prote  
aaas protein - Escherichia coli  
pathogenesis-related  
1-phosphatidylinositol

489,148 million cell updates/sec

Title: US-09-485-421-1  
Fitter score: 518  
Sequence: 1 MEAQADQDQDPYPPNWTI  
Starting table: BLASTME2  
GapOp: 10.0 , GapExt: 0.5

Searched:

219241 seqs, 76174552 residues

Minimum DB seq length: 0

Maximum DB seq length: 200000

Post-processing: Minimum Match 0.9

Maximum Match 1.00%

Listing first 45 Submatches

Database :  
1: PIR:f8; \*  
2: PIR:2; \*  
3: PIR:3; \*  
4: PIR:4; \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARY

Result No.	Score	Query	Description
1	45.9	804 6	vpr
2	45.4	87 6	vpr
3	44.8	93 6	vpr
4	44.5	85 9	vpr
5	44.5	35 2	vpr
6	40.2	96 1	vpr
7	24.8	47 9	vpr
8	24.8	47 9	vpr
9	24.7	47 7	vpr
10	24.5	47 4	vpr
11	24.3	47 0	vpr
12	24.4	45 6	vpr
13	22.4	43 2	vpr
14	22.5	42 8	vpr
15	21.5	41 4	vpr
16	21.9	41 5	vpr
17	21.9	40 5	vpr
18	21.9	39 4	vpr
19	15.3	29 5	vpr
20	19.1	19 1	vpr
21	97.5	18 8	vpr
22	93.5	18 1	vpr
23	92.5	17 6	vpr
24	90.5	17 5	vpr
25	84.5	16 3	vpr
26	84.5	16 3	vpr
27	84.5	11 2	vpr
28	83.4	11 2	vpr
29	83.4	11 2	vpr
30	79.5	11 2	vpr

RESULT 2  
Query Match 89.6%, Score 45.9; DR 27; Length 96;  
Best Local Similarity 87.5%; Prog. No.: 2; Gaps: 0;

Matches 84; Consistency: 7, Mismatches: 5; Indels: 0; Gaps: 0;  
P5: 1 MEAQADQDQDPYPPNWTI  
C: Species: human immunodeficiency virus type 1, HIV-1  
G: Accession: T09444  
P: Pari, S.; Vinters, H.V.; Akashi, T.; O'Bryan, W.A.; Chou, I.S.; Kyunggi, Y.; Kazar  
Submitted to the EMBL Data Library, July 1996  
A: Reference number: Z16673  
A: Accession: T09444  
A: Molecule type: DNA  
A: Residues: 1-96; SPAN: A  
A: Cross-references: EMBL:U66632; MID:91465777; PID:91465784  
C: Genetics: vpr

vpr protein - simi  
orf-X protein - simi  
vpx protein - huma  
vpx protein - huma  
vpx protein - huma  
probable membrane  
vpx protein - huma  
vpx protein - huma  
vpx protein - huma  
hypothetical prote  
beta glucosidase  
vpr protein - human  
hypothetical prote  
aaas protein - Escherichia coli  
pathogenesis-related  
1-phosphatidylinositol





RESULTS: The sequence of the 1407 nt<sup>1</sup> of SIV<sup>3</sup> is similar to that of the AIDS viruses except that it lacks the 3' terminal 122 nt<sup>2</sup>.

A; Reference number: A26747; M011087187627

A; Accession type: DNA

A; Length: 1407

A; Organism: Altis

C; Source: Altis

C; Keyword: AIDS; immunodeficiency

Query Match

Best local similarity

Score

Length

Detail

Mismatches

Indels

Gaps

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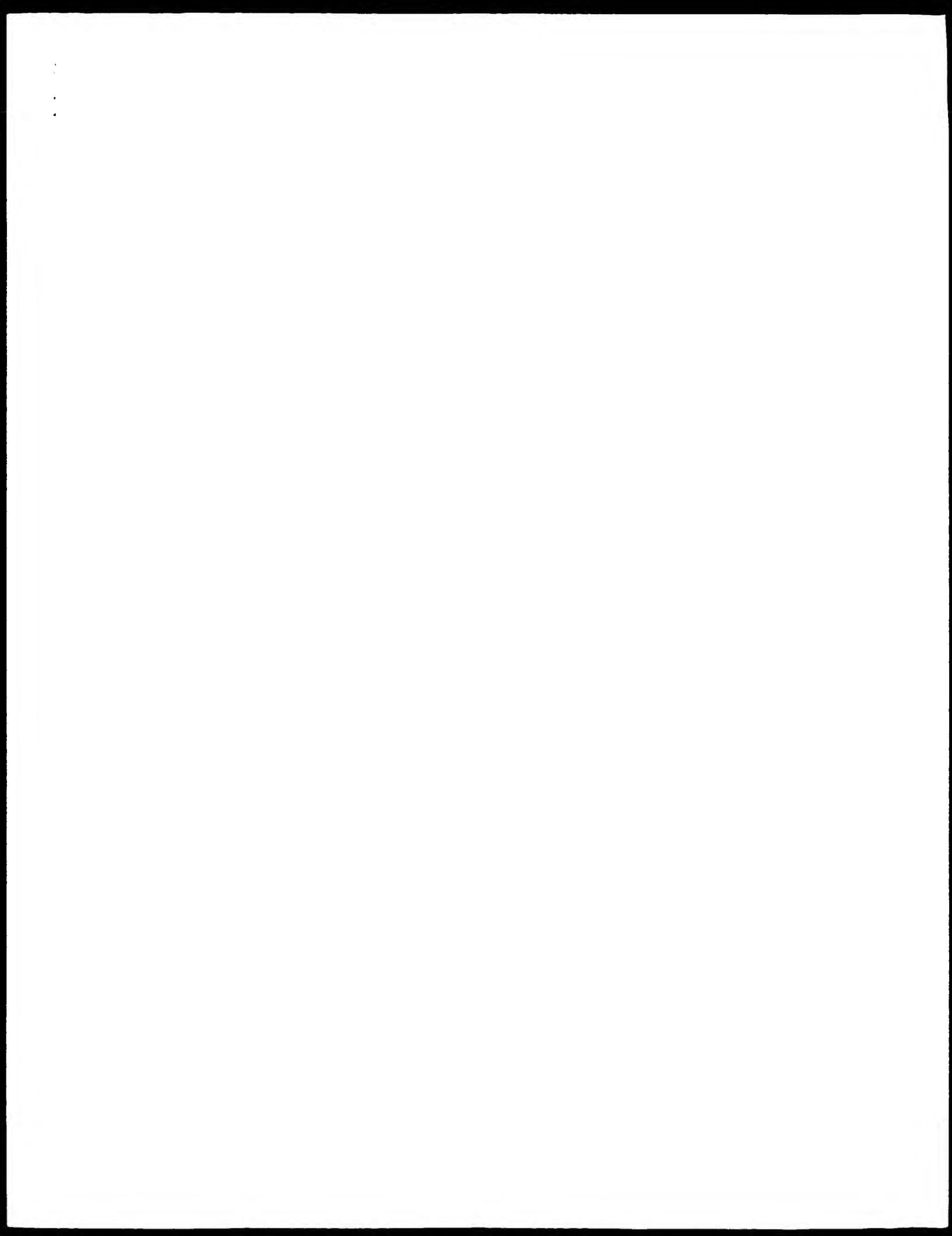
1

1

1</p

Sensitivity Match 43.4%; Score 214.5; DBI 1; Length 165;  
Fuzzy Local Similarity 48.9%; Pctd. No. 1.7a-16; Mismatches 24; Indels 7; Gaps 3;  
Matches 45; Conservative 16; Mismatches 24; Indels 7; Gaps 3;  
QY 2 EQUATIONARYRERWURKINGKRAVSKIIJKWIKSJOHITIVYKOMVIALU 60  
tb 7 EQUATIONARYRERWURKINGKRAVSKIIJKWIKSJOHITIVYKOMVIALU 60  
QY 61 KILLIWATIBERCRHRSGIHWURRLNG 92  
tb 65 KILLIWATIBERCRHRSGIHWURRLNG 92  
QY 66 KVKDRAFTHRAGHSIGG --- QYRG 92

Scan this comparison against 3, 2001, 13:22:05  
for more info.



©M protein - protein search, using sw model  
 protein sequence: 3, 2091, 13, 23, 17, 1, SWAPL + tree 9, 15, 5, 1, ends  
 (without alignments)  
 (93, 8, 89 million cell updates/second)

total score: 35,-0.9,485,-42,-1  
 protein score: 518  
 Sequence: 1 MEQALDQDPDPPEPPNWTL.....RASPLI3T1QCP2TPNRSK 96

Scoring table: BLUSUM62  
 GapP 10.0 , Gapext 0.5  
 searched: 6345 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 94435  
 Maximum DB seq length: 0  
 Maximum DB seq ID length: 2000000000

Post-processing: Minimum Match 0%

listing first 45 summaries

database : SwissProt 39;\*

pred. no.: the number of results predicted by choice to have a score greater than or equal to the score of the result being printed  
 and is derived by applying a p-value cutoff distribution

SUMMARIES

8

result No. score query start db id

1 47.0 36,7 95 1 VPR\_HV1BR

2 46.1 89,6 96 1 VPR\_HV1BR

3 46.4 89,6 96 1 VPR\_HV1BR

4 46.4 89,6 96 1 VPR\_HV1BR

5 45.9 89,6 96 1 VPR\_HV1BR

6 45.6 88,6 96 1 VPR\_HV1BR

7 45.4 87,6 96 1 VPR\_HV1BR

8 45.2 87,3 96 1 VPR\_HV1BR

9 44.8 86,6 97 1 VPR\_HV1BR

10 44.6 86,1 96 1 VPR\_HV1BR

11 44.5 86,0 97 1 VPR\_HV1AQ

12 44.5 85,9 96 1 VPR\_HV1MA

13 44.2 87,6 96 1 VPR\_SIVCZ

14 46.2 64,9 78 1 VPR\_HV1B1

15 45.8 69,1 78 1 VPR\_HV1B5

16 47.4 47,9 101 1 VPR\_SIVML

17 47.2 67,7 89 1 VPR\_HV1EVG

18 24.7 47,7 101 1 VPR\_SIVSP

19 24.5 47,9 101 1 VPR\_SIVML

20 24.5 47,3 123 1 VPR\_SIVML

21 26.5 47,9 105 1 VPR\_HV2NZ

22 22.6 43,7 105 1 VPR\_HV2SP

23 23.1 13,2 103 1 VPR\_HV2SP

24 22.5 42,9 104 1 VPR\_HV2TA

25 21.5 40,5 105 1 VPR\_HV2G1

26 21.1 40,7 105 1 VPR\_HV2H0

27 21.1 40,7 104 1 VPR\_HV2G1

28 20.7 40,0 105 1 VPR\_HV2A1

29 23.4 39,4 105 1 VPR\_HV2G1

30 18.7 36,1 105 1 VPR\_SIVSP

31 15,3 34,1 104 1 VPR\_SIVSP

32 11,3 23,9 119 1 VPR\_SIVML

33 10,4 105 1 VPR\_SIVML

34 10,0 105 1 VPR\_SIVML

35 9,7 105 1 VPR\_SIVML

36 9,3 5 105 1 VPR\_SIVML

37 9,2 5 105 1 VPR\_SIVML

38 9,0 5 105 1 VPR\_SIVML

39 84,5 16,3 112 1 VPR\_HV2G1

40 84,5 16,3 112 1 VPR\_SIVML

41 84,5 16,3 112 1 VPR\_HV2G1

42 83 16,0 112 1 VPR\_HV2G1

43 82,5 15,9 113 1 VPR\_HV2G1

44 81,5 15,7 111 1 VPR\_HV2G1

45 81,5 15,7 112 1 VPR\_SIVML

46 81,5 15,7 112 1 VPR\_SIVML

47 81,5 15,7 112 1 VPR\_SIVML

48 81,5 15,7 112 1 VPR\_SIVML

49 81,5 15,7 112 1 VPR\_SIVML

50 81,5 15,7 112 1 VPR\_SIVML

51 81,5 15,7 112 1 VPR\_SIVML

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60 81,5 15,7 112 1 VPR\_SIVML

61 81,5 15,7 112 1 VPR\_SIVML

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72 81,5 15,7 112 1 VPR\_SIVML

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81 81,5 15,7 112 1 VPR\_SIVML

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108 81,5 15,7 112 1 VPR\_SIVML

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188 81,5 15



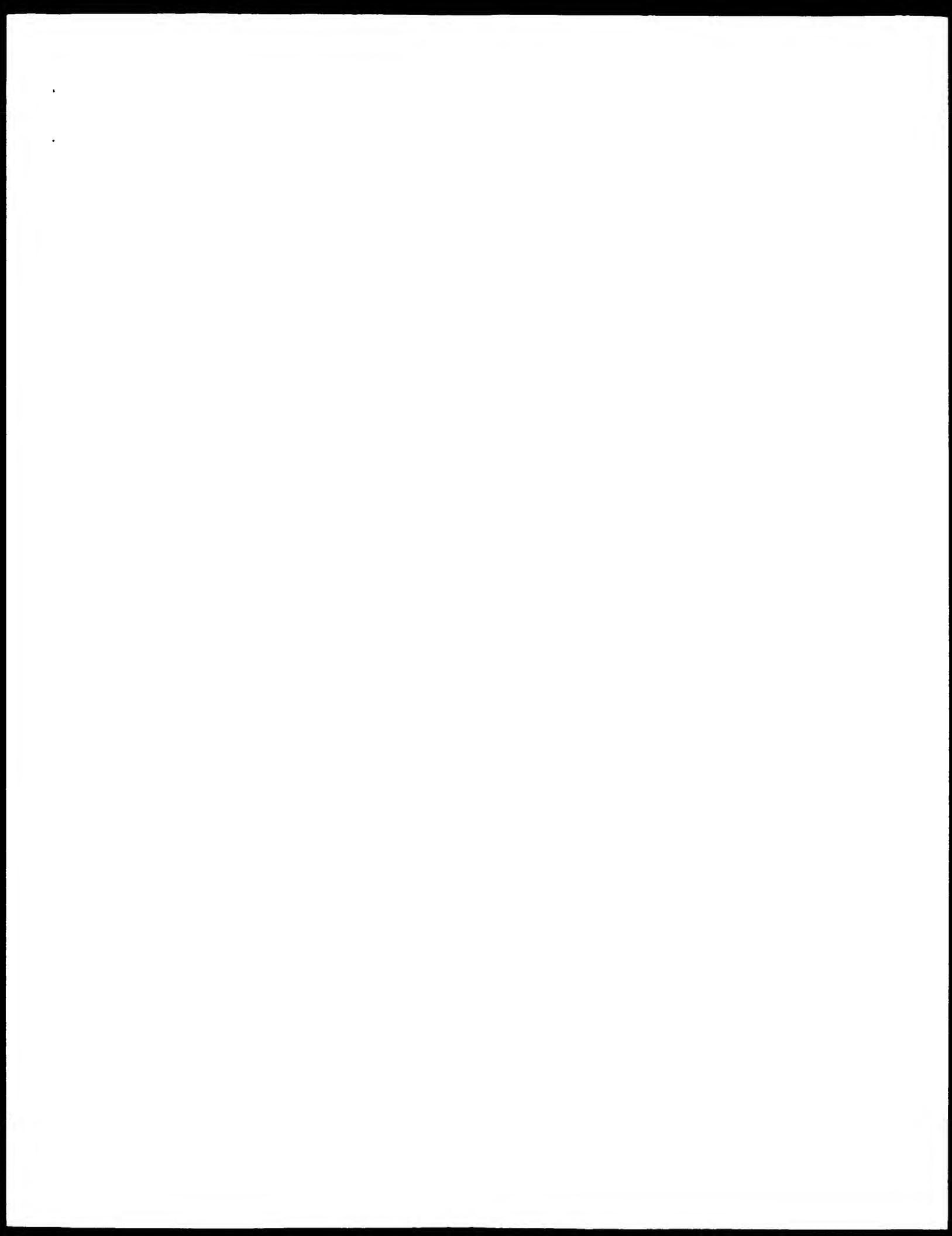
RESULT 6  
VIR\_HV1RH STANDARD PRT: 96 AA.  
ID 10554; 01-NOV-1988 (rel. 09, Created)  
ID 01-NOV-1988 (rel. 09, last sequence update)  
ID 01-JUL-1993 (rel. 26, last annotation update)  
DE VPRTEIN (R ORF PROTEIN).  
GN VFR.  
OS Human immunodeficiency virus type 1 (HIV-1) (HIV-1)  
OC Virtue Karplus Protein Database; PDB; 1992  
CX N912\_TAXID:11701;  
RN [1]  
RP SUBSTRATE: N.A.  
KA Starcich, B.R., Hahn, B.H., Shaw, G.M., McNeely, P.D., Modrow, S.,  
KA Wang, S., Park, P.S., Payne, W.P., Josephs, S.P., Gallo, R.C.,  
KA Submitted (xxxi-87) to the HIV data bank.  
CC  
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CC or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk).  
CC  
DR HIV; M17450; RAM5062.17;  
DR Interpret\_ProteinID; -  
DR AIDS; PDB0522; VPR; 1;  
DR PDB; PDB0522; VPR; 1;  
KW SEQUENCE 96 AA; 11378 MW; R293D;E2AE3724F; C8C64;  
KW AIDS; PDB0441; HIV1RVFX;  
KW  
PRT: PDB0522; VPR; 1;  
ID InterPro:IPRO000012; -  
ID Protein:IPRO0522; VPR; 1;  
ER PRTNIS; PRO0644; HIV1RVFX.  
KW  
SEQUENCE 96 AA; 11338 MW; 85KC4143; C9C744; C8C64;  
PRT: PDB0522; VPR; 1;  
ID InterPro:IPRO000012; -  
ID Protein:IPRO0522; VPR; 1;  
ER PRTNIS; PRO0644; HIV1RVFX.  
KW  
RESULT 7  
VIR\_HV1Z2 STANDARD PRT: 96 AA.  
AC P12519;  
ID 01-OCT-1989 (rel. 12, Created)  
ID 01-OCT-1989 (rel. 12, last sequence update)  
ID 01-OCT-1989 (rel. 26, last annotation update)  
RN 01-10-1993 (rel. 26, last annotation update)  
RA VPR.  
RA Theodore T. Buckler-White A.  
RA Submitted (NOV 1988) to the HIV data bank.  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC use. It can profit just as much as 1994 as its content is in no way  
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CC entities requires a license. Information: <http://www.ebi.ac.uk/swissprot/>  
CC or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk).  
CC  
DR HIV; M20639; RAM4536B.17;  
DR HIV; B2L2V; VPR522;  
ER Interpret\_ProteinID; -  
ID Protein:IPRO0522; VPR; 1;  
ER PRTNIS; PRO0644; HIV1RVFX.  
KW  
SEQUENCE 96 AA; 11380 MW; 85KC4143D959A944; C9C744;  
KW  
PRT: PDB0522; VPR; 1;  
ID InterPro:IPRO000012; -  
ID Protein:IPRO0522; VPR; 1;  
ER PRTNIS; PRO0644; HIV1RVFX.  
KW  
PRT: PDB0522; VPR; 1;  
ID InterPro:IPRO000012; -  
ID Protein:IPRO0522; VPR; 1;  
ER PRTNIS; PRO0644; HIV1RVFX.  
KW  
SEQUENCE 96 AA; 11378 MW; R293D;E2AE3724F; C8C64;  
PRT: PDB0522; VPR; 1;  
ID InterPro:IPRO000012; -  
ID Protein:IPRO0522; VPR; 1;  
ER PRTNIS; PRO0644; HIV1RVFX.







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RE: STRAIN FROM N.A.

KG: STRAIN-PATIENT 3799(G-5A); TISSUE-BLOOD;

RA: Michael N.L.;

RI: Submitted (AF 1555) to the EMBL, DDBJ, and GenBank databases

DR: EML: U24483; AAC70654; 1; -;

DR: InterPro: IPR00522; VPR: 1;

DR: PRINS: PRO044; HVWPPVX;

SEQUENCE: 96 AA: 11365 MW: 3654EA9EAB825 CDS: 4;

Query Match: 91.5%; Score 474; DB 14; Length 96;

Best Local Similarity: 91.5%; Pred. No.: 4; Gaps: 0;

Matches: 88; Consistency: 3; Mismatches: 5; Index: 0; Gaps: 0;

QY: 1 MEAFAFPPGDPPEPFWILLKLLKAVPHPFWHNSLQVLYTSPWENAL 60

DB: 1 MEAFAFPPGDPPEPFWILLKLLKAVPHPFWHNSLQVLYTSPWENAL 60

DR: InterPro: IPR00522; VPR: 1;

DR: PRINS: PRO044; HVWPPVX;

DR: GEODICE: 96 AA: 11346 MW: 3654EA9EAB825 CDS: 4;

DR: InterPro: IPR00522; VPR: 1;

DR: PRINS: PRO044; HVWPPVX;

DR: GEODICE: 96 AA: 11346 MW: 3654EA9EAB825 CDS: 4;

DR: InterPro: IPR00522; VPR: 1;

DR: PRINS: PRO044; HVWPPVX;

DR: GEODICE: 96 AA: 11346 MW: 3654EA9EAB825 CDS: 4;

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DR: PRINS: PRO044; HVWPPVX;

DR: GEODICE: 96 AA: 11346 MW: 3654EA9EAB825 CDS: 4;

DR: InterPro: IPR00522; VPR: 1;

DR: PRINS: PRO044; HVWPPVX;

DR: GEODICE: 96 AA: 11346 MW: 3654EA9EAB825 CDS: 4;

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DR: PRINS: PRO044; HVWPPVX;

DR: GEODICE: 96 AA: 11346 MW: 3654EA9EAB825 CDS: 4;

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DR: PRINS: PRO044; HVWPPVX;

DR: GEODICE: 96 AA: 11346 MW: 3654EA9EAB825 CDS: 4;

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DR: GEODICE: 96 AA: 11346 MW: 3654EA9EAB825 CDS: 4;

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DR: PRINS: PRO044; HVWPPVX;

DR: GEODICE: 96 AA: 11346 MW: 3654EA9EAB825 CDS: 4;

DR: InterPro: IPR00522; VPR: 1;

DR: PRINS: PRO044; HVWPPVX;

DR: GEODICE: 96 AA: 11346 MW: 3654EA9EAB825 CDS: 4;

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DR: PRINS: PRO044; HVWPPVX;

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DR: PRINS: PRO044; HVWPPVX;

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DR: PRINS: PRO044; HVWPPVX;

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DR: PRINS: PRO044; HVWPPVX;

DR: GEODICE: 96 AA: 11346 MW: 3654EA9EAB825 CDS: 4;

DR: InterPro: IPR00522; VPR: 1;

VIRUS: Retried viruses; Sattlerviridae; Lentivirus.

DR: NCBI\_TAXID=11676;

RN: [1]

RE: STRAIN-PATIENT 0583, HOMOSEXUAL, DUTCH;

RA: Kuijken L., Cornelisse, E., Zondervan F., Hartman S., Gibbs J.,

RI: Goudsmit J., J. Gen. Virol. 010-01(1996);

RA: J. Gen. Virol. 010-01(1996);

DR: EMLB: 26849; JAVEL872; 1; -;

DR: InterPro: IPR00522; -;

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DR: GEODICE: 96 AA: 11346 MW: 3654EA9EAB825 CDS: 4;

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DR: GEODICE: 96 AA: 11346 MW: 3654EA9EAB825 CDS: 4;

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DR: PRINS: PRO044; HVWPPVX;

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DR: PRINS: PRO044; HVWPPVX;

DR: GEODICE: 96 AA: 11346 MW: 3654EA9EAB825 CDS: 4;

DR: InterPro: IPR00522; VPR: 1;





Wed Oct 3 13:40:06 2001

us-09-485-421-1.rspt

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## APPENDICES

Result No.	Score	Uniq Match	Length	DB ID	Description
1	20	100	0	78	HIV Vpr protein, a
2	25	150	0	20	HIV Vpr protein, a
3	20	100	0	96	HIV Vpr protein, a
4	20	100	0	20	HIV Vpr protein, a
5	20	100	0	96	HIV Vpr protein, a
6	20	100	0	96	HIV Vpr protein, a
7	20	100	0	96	HIV Vpr protein, a
8	20	100	0	95	HIV Vpr protein, a
9	20	100	0	96	HIV Vpr protein, a
10	20	100	0	96	HIV Vpr protein, a
11	20	100	0	96	HIV Vpr protein, a

SUMMARY

higher than or equal to the score at the result being printed, derived by analysis of the total score distribution.

score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.









protein; Mat. 4; Score: 207; DB: 177; Length: 495;  
Best local similarity: 100.0%; Prcd. No.: 12; Mismatches: 0; Indels: 0; Gaps: 0;

XX DE Fragment of native Vpr protein from HIV-1 LAI strain isolate.

XX KW Native Vpr protein; HIV-1 LAI strain isolate; Treatment: Infection; replication; written assembly; functional integrity.

XX OS Human immunodeficiency virus type 1.

XX PN W94607741 A1.

XX XX 14-MAR-1996.

XX XX 07-SEP-1997; 95W-1A10510.

XX PR 07-SEP-1994; 940JS-0301945.

XX PA (UVM) UNIV MONTREAL.

XX XX 11 Borquet D., Chretien F., Cohen FA., Pianac-Kobinger G;

XX PT Yao X;

XX WPB: 1996, 171015/17.

PT Targeting mature HIV virion(s) using HIV Vpr, Vpx or p6 proteins - for detecting structural organisation or function or for inhibiting replication

XX PS claim 11; pages 44-45; 68pp; English.

XX CC The present sequence is a fragment of the native Vpr protein from the HIV-1 LAI strain isolate, which can be used to prevent viral replication by interfering with the protein interactions responsible for Vpr incorporation into the mature HIV-1 genome.

XX SQ sequence 72 AA;

WPB: 1999, 181134/15.

XX C-terminal fragment of a recombinant HIV-1 Vpr protein concatenated to a therapeutic peptide; used for inhibiting cell proliferation and transducing lymphoproliferative disease.

XX EG 180102: E91; RefSeq: RefSeq.

XX PT Targeting mature HIV virion(s); a recombinant sequence consisting of a C-terminal fragment of HIV-1 Vpr protein concatenated to a therapeutic peptide; used for inhibiting cell proliferation and transducing lymphoproliferative disease.

XX CC The present invention describes a recombinant sequence consisting of HIV-1 Vpr protein concatenated to a therapeutic peptide; used for inhibiting cell proliferation and transducing lymphoproliferative disease. The composition can be used to treat HIV-1 infected individuals who has a hyperplastic therapeutic disease. The HIV-1 Vpr protein has a recombinant peptide, which is formed by joining components that inhibit Vpr protein functions, e.g., formation of pores or the properties. The present sequence represents an HIV-1 protein sequence.

XX DE Sequence: 95W-1A10510.

RESULT 1d

AY54250 ID AY54250 standard; Protein: 72 AA.

XX AC AY54250;

XX DT 17-JUL-2000 (first entry)

XX DE SIV Vpr Protein; SEQ ID No:4.

XX KW HIV-1 Vpr; virion: Vpr; Vpx; p6; chimeric; infection; anti-HIV; gene therapy.

XX OS Simian immunodeficiency virus.

PN US6043091 A.

XX 28 MAR 2000.

XX DE 07-SEP-1995; 95W-0624694.

XX KK 07-SEP-1994; 940JS-0301945.

XX (UVM) UNIV MONTREAL.

XX PA Yao X., Pianac-Kobinger G., Chretien F.A., Borquet D.

XX PN W94607741 A1.



Wed Oct 3 13:40:06 2001

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#### SUMMARIES

ALIGNMENTS



US-08-401-915-1

Query Match Similarity 95.0%; Score 10; DR 2; length 96;

Best Local Similarity 100.0%; Prod. No. 2.5c-11; Mismatches 0; Indexes 0; Gaps 0; Oligos 0;

Match 2 WTHLEEKNEAVHWRP 29 1a 1b WTHLEEKNEAVHWRP 36

RESULT 5  
US-08-524-694A-1  
Sequence 1, Application US/08524694A  
Patent No. 604308  
GENERAL INFORMATION:  
APPLICANT: GAJIN, ERIC A.  
APPLICANT: BURGER, DOMINIQUE  
APPLICANT: CHETEONE, FLORENT  
APPLICANT: PICHAC KOMBIER, GARY  
TITLE OF INVENTION: PROTEIN TARGETING INTO HIV VIRIONS BASED  
TITLE OF INVENTION: ON HIV-1 VPR FUSION MOLECULES  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSE: KLAUDEM & JACKSON  
STREET: Continental Plaza, 411 Hackensack Avenue  
CITY: Hackensack  
STATE: N.J.  
COUNTRY: U.S.A.  
ZIP: 07601COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
OPERATING SYSTEM: PC BUSINESS DOS

SOFTWARE: PATENT RELEASE #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: 58779524694A  
FILING DATE: September 7, 1995  
CLASSIFICATION: 514ATTORNEY/AGENT INFORMATION:  
NAME: JACKSON, David A.  
PRACTITIONER NUMBER: 26-242  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 732-7040FILING DATE: 28-Aug-1996  
CLASSIFICATION:  
NAME: FRIED, Allan H.REGISTRATION NUMBER: 31-253  
REFERENCE/COPYRIGHT NUMBER: 119-907TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 732-7040

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:  
LENGTH: 96 amino acids  
TYPE: amino acidTOPOLOGY: Linear  
HYDROPHOBIC: N

US-08-704-856-2-15

RESULT 6  
US-08-704-856-2-15  
Sequence 15, Application US/08704856C  
Patent No. 6042842  
GENERAL INFORMATION:  
APPLICANT: KATZ, Jean-Louis  
APPLICANT: SOKOL, Renate  
APPLICANT: BULTER, Klaus  
APPLICANT: CORNAT, Isabelle  
APPLICANT: METZ, Gunther  
APPLICANT: DUFOUR, Jean  
TITLE OF INVENTION: AN ELLIOPROTEIN AND REBISSES  
TITLE OF INVENTION: AN ELLIOPROTEIN AND REBISSES  
NUMBER OF SEQUENCES: 258  
CORRESPONDENCE ADDRESS:  
ADDRESS: Brantie & Edwards LLP  
SUITE: 1155 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036-2841COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
OPERATING SYSTEM: DOSCURRENT APPLICATION DATA:  
APPLICATION NUMBER: 58779524694A-1SEQUENCE CHARACTERISTICS:  
LENGTH: 96 amino acids  
TYPE: amino acidTOPOLOGY: Linear  
HYDROPHOBIC: N

US-08-524-694A-1

RESULT 7  
US-08-940-095-196  
Sequence 196, Application US/08940095  
Patent No. 6004925  
GENERAL INFORMATION:  
APPLICANT: LASSON, Jean-Louis  
APPLICANT: SOKOL, Renate  
APPLICANT: BULTER, Klaus  
APPLICANT: CORNAT, Isabelle  
APPLICANT: METZ, Gunther  
APPLICANT: DUFOUR, Jean  
TITLE OF INVENTION: AN ELLIOPROTEIN AND REBISSES  
TITLE OF INVENTION: AN ELLIOPROTEIN AND REBISSES  
NUMBER OF SEQUENCES: 258  
CORRESPONDENCE ADDRESS:  
ADDRESS: Brantie & Edwards LLP  
SUITE: 1155 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036-2841COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
OPERATING SYSTEM: DOSCURRENT APPLICATION DATA:  
APPLICATION NUMBER: 58779524694A-1SEQUENCE CHARACTERISTICS:  
LENGTH: 96 amino acids  
TYPE: amino acidTOPOLOGY: Linear  
HYDROPHOBIC: N

US-08-524-694A-1



LENGTH: 18 amino acids  
TYPE: amino acid  
STRANEDNESS: single  
TOPOLACY: linear

MOLECULE TYPE: No. 6046166e  
NAME/KEY: 5  
LOCATION: 1..18  
OTHER INFORMATION: N-terminal acetylated and  
THEIR INFORMATION: C-terminal amidated

US-08-940-096-196

Query Match Similarity 40.0%; Score 8; DB 3; Length 18;  
Matches 8; Location 1..18; Other Information: Misaligned; Indels 0; Gaps 0;

QY

5 ELAERIK 12  
DQ 8 ELAERIK 15

DB

8 ELAERIK 14

ID

OTHER INFORMATION: N-terminal acetylated and  
OTHER INFORMATION: C-terminal amidated

US-08-940-096-253

Query Match Similarity 40.0%; Score 7; DB 3; Length 16;  
Matches 7; Location 1..16; Other Information: Misaligned; Indels 0; Gaps 0;

QY

5 ELAERIK 11  
DQ 8 ELAERIK 14

DB

ID



TITLE OF INVENTION: ANG TIEER USE TO TREAT CYSTICEROSIS DISORDERS  
 NUMBER OF SEQUENCES: 2<sup>nd</sup>  
 CORRESPONDENCE ADDRESS:  
 APPLICANT: Penno & Edmonds LLP  
 STREET: 1155 Avenue of the Americas  
 STATE: NY  
 ZIP: 10036-2811  
 COUNTRY: USA  
 COMPUTER RELATED FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSeq Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US08940095  
 FILING DATE: 29 SEP 1997  
 CLASSIFICATION: 514  
 PRIORITY APPLICATION DATA:  
 PRIORITY NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Corruzzelli, Laura A.  
 REFERENCE/PATENT NUMBER: 5594166 0/04 4/93  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 650-493-4945  
 TELEFAX: 650-493-5556  
 FAX: 650-493-4945  
 MOLECULE TYPE: Peptide  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 18 amino acids  
 TYPE: amino acid  
 STRANGENESS: single  
 TOPOLOGY: Linear  
 PEPTIDE: Other  
 FEATURES:  
 NAME: Other  
 LOCATION: 1...18  
 OTHER INFORMATION: N-terminal acetylated and  
 C-terminal amidated  
 US-08-940-095-192

SEARCH Match 35,08%; Score 7; DB 3; Length 18;  
 Best local Similarity 100.0%; Pred. No. 0.85; Mismatches 0; Gaps 0;  
 Matches 7; Conservative 0; Miscons 0; Indels 0;  
 OTHER INFORMATION: C-terminal amidated  
 US-08-940-095-193

SEARCH Match 35,08%; Score 7; DB 3; Length 18;  
 Best local Similarity 100.0%; Pred. No. 0.85; Mismatches 0; Gaps 0;  
 Matches 7; Conservative 0; Miscons 0; Indels 0;  
 OTHER INFORMATION: C-terminal amidated  
 US-08-940-095-194

SEARCH Match 35,08%; Score 7; DB 3; Length 18;  
 Best local Similarity 100.0%; Pred. No. 0.85; Mismatches 0; Gaps 0;  
 Matches 7; Conservative 0; Miscons 0; Indels 0;  
 OTHER INFORMATION: C-terminal amidated  
 Job time: 124 sec.

RESULT 15  
 US-08-940-095-194  
 Sequence 193, Application US/08940095  
 Patent No. 604925  
 GENERAL INFORMATION:  
 APPLICANT: Tasseux, Jean-Louis  
 APPLICANT: Sekoul, Renate  
 APPLICANT: Butner, Klaus  
 APPLICANT: Cortot, Isabelle  
 APPLICANT: Metz, Gunther  
 APPLICANT: Butner, Klaus  
 TITLE OF INVENTION: A polypeptide A-1 agonist  
 NUMBER OF SEQUENCES: 2<sup>nd</sup>  
 CORRESPONDENCE ADDRESS:  
 APPLICANT: Penno & Edmonds LLP  
 STREET: 1155 Avenue of the Americas  
 CITY: New York  
 STATE: NY  
 COUNTRY: USA

ZIP: 10036-2811  
 COMPUTER RELATED FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSeq Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US08940095  
 FILING DATE: 29 SEP 1997  
 CLASSIFICATION: 514  
 PRIORITY APPLICATION DATA:  
 PRIORITY NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Corruzzelli, Laura A.  
 REFERENCE/PATENT NUMBER: 5594166 0/04 4/93  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 650-493-4945  
 TELEFAX: 650-493-5556  
 FAX: 650-493-4945  
 MOLECULE TYPE: Peptide  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 18 amino acids  
 TYPE: amino acid  
 STRANGENESS: single  
 TOPOLOGY: Linear  
 PEPTIDE: Other  
 FEATURES:  
 NAME: Other  
 LOCATION: 1...18  
 OTHER INFORMATION: N-terminal acetylated and  
 C-terminal amidated  
 US-08-940-095-193

wed oct 3 13:40:06 2001

us-09-485-421-1\_copy\_17\_36.rai

Genetic version 4.5  
Copyright (c) 1993 - 2000 Computer Ltd.

!M protein - protein in search. us191 sw mode!  
Run on: october 3, 2001, 13:24:32 ; Search time 22.56 seconds  
Sequence: 1 WILDELEKSKNARWHRP 20  
Scoring table: sln03  
gapop 60.0 , gapext 60.0

Title: US-09-485-421-1\_copy\_17\_36  
integer score: 25  
1 WILDELEKSKNARWHRP 20  
67.51 Million cell updates/sec

Searched: 219241 seqs, 76174552 residues

Word size : 0

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Minimum DP seq length: 20

Post-processing: sorting first 45 summaries

Database : p19\_684,\*  
1: P19\_684,\*  
2: P19\_684,\*  
3: P19\_684,\*  
4: P19\_684,\*

Pred\_N0 is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Length	DP	Description
1	19	95.0	96	VPR protein - human immunodeficiency virus type I (strain JKV)
2	14	70.0	96	VPR protein - simian immunodeficiency virus type I, HIV-1
3	10	50.0	95	VPR protein - human immunodeficiency virus type I, HIV-1
4	10	50.0	96	VPR protein - human immunodeficiency virus type I, HIV-1
5	19	50.6	96	VPR protein - human immunodeficiency virus type I, HIV-1
6	6	50.0	97	VPR protein - human immunodeficiency virus type I, HIV-1
7	8	40.0	623	VPR protein - human immunodeficiency virus type I, HIV-1
8	8	40.0	635	VPR protein - simian immunodeficiency virus type I, HIV-1
9	8	40.0	635	VPR protein - simian immunodeficiency virus type I, HIV-1
10	8	40.0	635	VPR protein - simian immunodeficiency virus type I, HIV-1
11	9	35.0	150	VPR protein - human immunodeficiency virus type I, HIV-1
12	9	35.0	157	VPR protein - human immunodeficiency virus type I, HIV-1
13	7	35.0	222	VPR protein - human immunodeficiency virus type I, HIV-1
14	7	35.0	295	VPR protein - human immunodeficiency virus type I, HIV-1
15	7	35.0	459	VPR protein - human immunodeficiency virus type I, HIV-1
16	7	35.0	471	VPR protein - human immunodeficiency virus type I, HIV-1
17	7	35.0	532	VPR protein - human immunodeficiency virus type I, HIV-1
18	7	35.0	535	VPR protein - human immunodeficiency virus type I, HIV-1
19	7	35.0	546	VPR protein - human immunodeficiency virus type I, HIV-1
20	7	35.0	640	VPR protein - human immunodeficiency virus type I, HIV-1
21	9	35.0	647	VPR protein - human immunodeficiency virus type I, HIV-1
22	7	35.0	749	VPR protein - human immunodeficiency virus type I, HIV-1
23	7	35.0	968	VPR protein - human immunodeficiency virus type I, HIV-1
24	7	35.0	972	VPR protein - human immunodeficiency virus type I, HIV-1
25	7	35.0	1005	VPR protein - human immunodeficiency virus type I, HIV-1
26	7	35.0	1169	VPR protein - human immunodeficiency virus type I, HIV-1
27	4	38.0	17014	VPR protein - human immunodeficiency virus type I, HIV-1
28	6	52.0	42196	VPR protein - human immunodeficiency virus type I, HIV-1
29	6	52.0	53529	VPR protein - human immunodeficiency virus type I, HIV-1

## ALIGNMENTS

0	6	30.0	70	2	H64511	hypothetical prote
31	6	30.0	70	2	A75134	hypothetical prote
42	6	30.0	92	2	B69177	probable glutaredo
43	6	30.0	107	2	B71010	hypothetical prote
34	6	40.0	125	2	B15619	hypothetical prote
45	6	40.0	145	2	A29594	hypothetical prote
36	6	30.0	136	2	I12823	hypothetical prote
37	6	30.0	138	2	G82116	thioredoxin-like
38	6	30.0	145	2	S25220	replication prote
39	6	30.0	150	2	F7019	transcription regu
40	6	40.0	152	2	C8211	hypothetical prote
41	6	30.0	153	2	S29552	interleukin-2-like
42	6	30.0	155	2	S1488	interleukin-2-like
43	6	30.0	155	2	I4513	interleukin-2-like
44	6	30.0	157	2	A71337	hypothetical prote
45	6	30.0	171	1	B60010	early ELA 20k prote





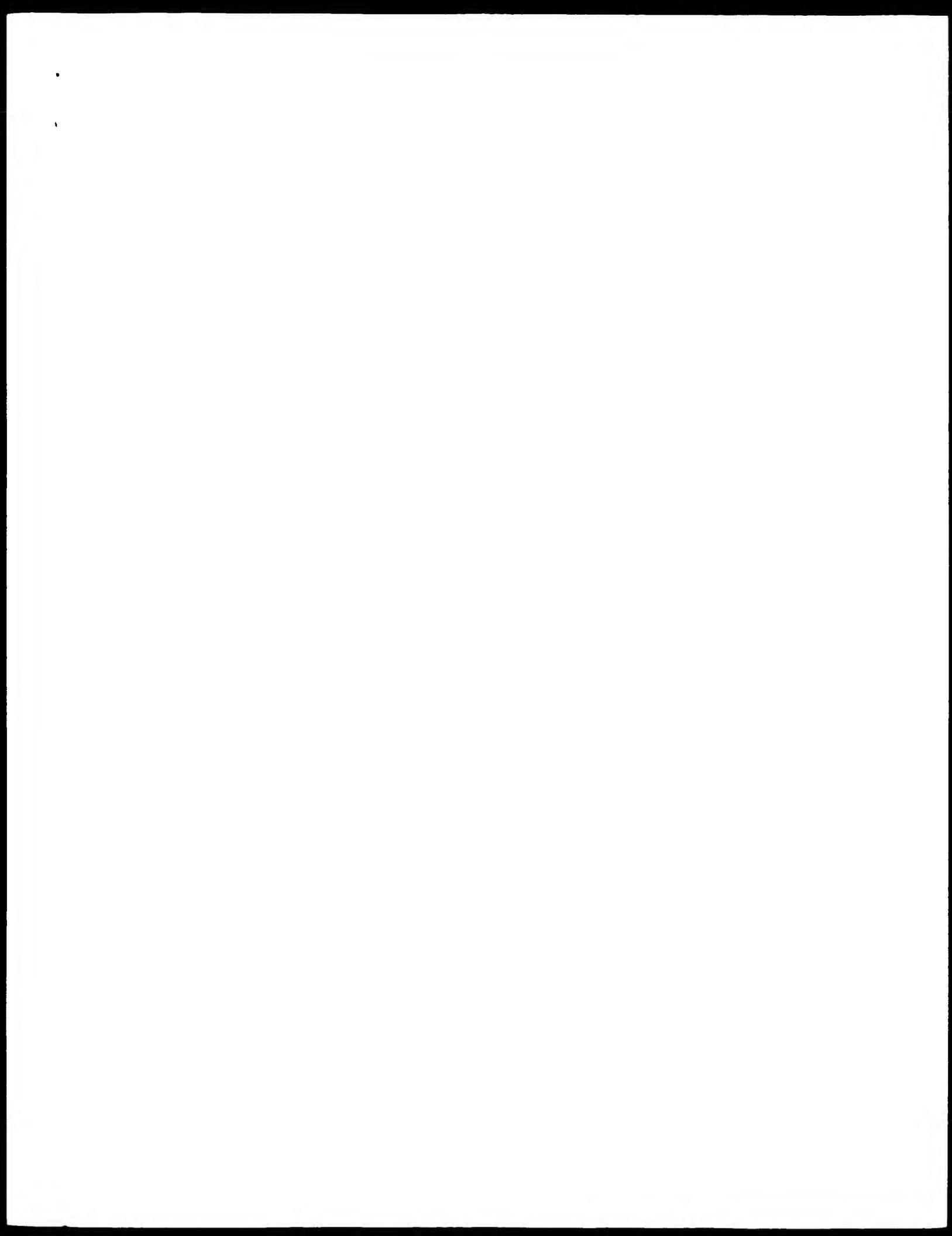


Wed Oct 3 13:40:07 2001

us-09-485-421-1\_copy\_17\_36.rpr

Page 5

Search completed: October 3, 2001, 13:24:03  
Job time: 271 sec



temcore version 4.5  
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Run on: October 3, 2001 13:25:22 ; search time 33.2 seconds  
(without alignments)

Scoring tables: effon gapep gapext 60.0

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: listing first 45 summaries

Database : SPREMBL\_16;\*

1: sp\_bacteria;\*

2: sp\_bacteria;\*

3: sp\_fungi;\*

4: sp\_human;\*

5: sp\_invertebrate;\*

6: sp\_mammal;\*

7: sp\_phage;\*

8: sp\_prokaryote;\*

9: sp\_phage;\*

10: sp\_plant;\*

11: sp\_rickettsia;\*

12: sp\_unclassified;\*

13: sp\_vertebrate;\*

14: sp\_virus;\*

15: sp\_virus;\*

16: sp\_virus;\*

17: sp\_virus;\*

18: sp\_virus;\*

19: sp\_virus;\*

20: sp\_virus;\*

21: sp\_virus;\*

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250: sp\_v

RESULTS  
Human immunodeficiency virus type 1;  
retroviridae; lentivirus.

NCBI TaxID:11676;

RENAME [1]

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RENAME [2]

SEQUENCE FROM N.A.

RENAME [3]

SEQUENCE FROM N.A.

RENAME [4]

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RENAME [5]

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RENAME [6]

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RENAME [29]

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RENAME [31]

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RENAME [32]

SEQUENCE FROM N.A.

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Q91Q92 PRELIMINARY; PRT; 96 AA.  
ID Q91Q92; PRELIMINARY; PRT; 96 AA.  
AC Q91Q92; PRELIMINARY; PRT; 96 AA.  
DE 01-OCT-2000 (REMOVED); 15, (last sequence update)  
DT 01-OCT-2000 (REMOVED); 15, (last annotation update)  
ID Q91Q92; PRELIMINARY; PRT; 96 AA.  
DE VPR PROTEIN.  
GN VPR.  
OS Human immunodeficiency virus type 1.  
OC Retroviral viruses; Retroviridae; Lentivirus.  
CK NCBI\_TaxID:11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
PK STRAIN=PATENT; PubMed 19981687;  
PK MEDLINE=20338046; PubMed 19981687;  
RN Yamada T., Yamamoto A.;  
RE "Comparison of proviral accessory genes between long-term nonproliferators and progressors of human immunodeficiency virus type 1 infection."  
RL Arch. Virol. 145:1021-1027(2000).  
DR EMBL:AB04554; RIBN:94001; 1-  
DR InterPro: IPR00012;-  
DR InterPro: IPR00154;-  
DR Pfam:PF0052; VIR: 1;  
DR PRINS; PR0044; BLWVNPX.  
DR Project: PR001667;-; 1-  
DR STRAIN= 06 AA; 11396 MW; 3171471E85KMEPFCRC64;  
SQ

RESULT 5  
089598 PRELIMINARY; PRT; 37 AA.  
ID 089598; PRELIMINARY; PRT; 37 AA.  
AC 089598; PRELIMINARY; PRT; 37 AA.  
DE 01-NOV-1996 (REMOVED); 01, (last sequence update)  
DT 01-NOV-1996 (REMOVED); 01, (last annotation update)  
ID HIV-1 DNA FOR GAG, PRO, VIF, VPR, RTR, TAT, ENV, VPI.  
GN VPR.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
CK NCBI\_TaxID:11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
PK STRAIN=IM21; cloyd M.W., Moore B.E.;  
KL Submitted (JUN 1996) to the EMBL, Genbank, DDBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
PK STRAIN=IM21;  
RA Katoch V.;  
KL Submitted (JUN 1996) to the EMBL, Genbank, DDBJ databases.  
DR EMBL:086069; RIBN:12991; 1-  
DR EMBL:086067; RIBN:12991; 1-  
DR InterPro: IPR00012;-  
DR InterPro: IPR0052; VIR: 1;  
DR Pfam:PF0052; VIR: 1;  
DR STRAIN= 07 AA; 4168 MW; 3171471E85KMEPFCRC64;

QUERY Match: 100.0%; Score: 100.0%; Length: 96;  
Best Local Similarity: 100.0%; Pred. No.: 2; Seq: 10;  
Matches: 19; conservative: 0; Mismatches: 0; Indexes: 0; Gaps: 0;

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Matches: 19; conservative: 0; Mismatches: 0; Indexes: 0; Gaps: 0;

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Best Local Similarity: 100.0%; Pred. No.: 2; Seq: 10;  
Matches: 19; conservative: 0; Mismatches: 0; Indexes: 0; Gaps: 0;

QUERY Match: 100.0%; Score: 100.0%; Length: 96;  
Best Local Similarity: 100.0%; Pred. No.: 2; Seq: 10;  
Matches: 19; conservative: 0; Mismatches: 0; Indexes: 0; Gaps: 0;

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Best Local Similarity: 100.0%; Pred. No.: 2; Seq: 10;  
Matches: 19; conservative: 0; Mismatches: 0; Indexes: 0; Gaps: 0;

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Best Local Similarity: 100.0%; Pred. No.: 2; Seq: 10;  
Matches: 19; conservative: 0; Mismatches: 0; Indexes: 0; Gaps: 0;

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Matches: 19; conservative: 0; Mismatches: 0; Indexes: 0; Gaps: 0;

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Matches: 19; conservative: 0; Mismatches: 0; Indexes: 0; Gaps: 0;

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Best Local Similarity: 100.0%; Pred. No.: 2; Seq: 10;  
Matches: 19; conservative: 0; Mismatches: 0; Indexes: 0; Gaps: 0;

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Best Local Similarity: 100.0%; Pred. No.: 2; Seq: 10;  
Matches: 19; conservative: 0; Mismatches: 0; Indexes: 0; Gaps: 0;

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Best Local Similarity: 100.0%; Pred. No.: 2; Seq: 10;  
Matches: 19; conservative: 0; Mismatches: 0; Indexes: 0; Gaps: 0;

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Matches: 19; conservative: 0; Mismatches: 0; Indexes: 0; Gaps: 0;

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Best Local Similarity: 100.0%; Pred. No.: 2; Seq: 10;  
Matches: 19; conservative: 0; Mismatches: 0; Indexes: 0; Gaps: 0;

QUERY Match: 100.0%; Score: 100.0%; Length: 96;  
Best Local Similarity: 100.0%; Pred. No.: 2; Seq: 10;  
Matches: 19; conservative: 0; Mismatches: 0; Indexes: 0; Gaps: 0;

QUERY Match: 100.0%; Score: 100.0%; Length: 96;  
Best Local Similarity: 100.0%; Pred. No.: 2; Seq: 10;  
Matches: 19; conservative: 0; Mismatches: 0; Indexes: 0; Gaps: 0;

QUERY Match: 100.0%; Score: 100.0%; Length: 96;  
Best Local Similarity: 100.0%; Pred. No.: 2; Seq: 10;  
Matches: 19; conservative: 0; Mismatches: 0; Indexes: 0; Gaps: 0;

QUERY Match: 100.0%; Score: 100.0%; Length: 96;  
Best Local Similarity: 100.0%; Pred. No.: 2; Seq: 10;  
Matches: 19; conservative: 0; Mismatches: 0; Indexes: 0; Gaps: 0;

QUERY Match: 100.0%; Score: 100.0%; Length: 96;  
Best Local Similarity: 100.0%; Pred. No.: 2; Seq: 10;  
Matches: 19; conservative: 0; Mismatches: 0; Indexes: 0; Gaps: 0;

QUERY Match: 100.0%; Score: 100.0%; Length: 96;  
Best Local Similarity: 100.0%; Pred. No.: 2; Seq: 10;  
Matches: 19; conservative: 0; Mismatches: 0; Indexes: 0; Gaps: 0;

QUERY Match: 100.0%; Score: 100.0%; Length: 96;  
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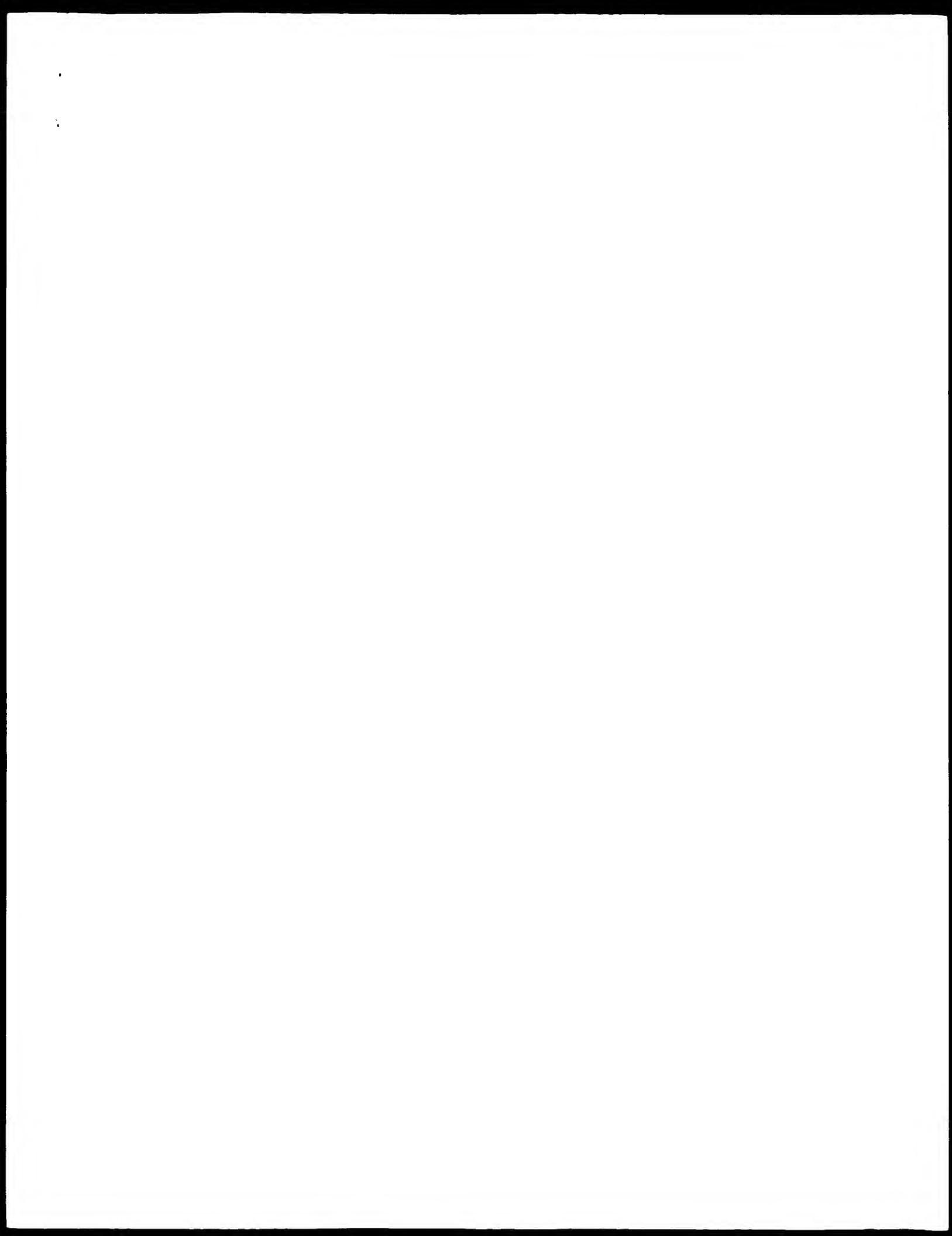
QUERY Match: 100.0%; Score: 100.0%; Length: 96;  
Best Local Similarity: 100.0%; Pred. No.: 2; Seq: 10;  
Matches: 19; conservative: 0; Mismatches: 0; Indexes: 0; Gaps: 0;

QUERY Match: 100.0%; Score: 100.0%; Length: 96;  
Best Local Similarity: 100.0%; Pred. No.: 2; Seq: 10;  
Matches: 19; conservative: 0; Mismatches: 0; Indexes: 0; Gaps: 0;

Q7	2 WTLEELFEKNEAVHPRP 20	Q7	2 WTLEELFEKNEAVHPRP 20
ID	Q9WQ07	ID	Q9WQ07
AC	Q9WQ07;	AC	Q9WQ07;
DT	01-NOV-1999 (TREMBREL, 12; created)	DT	01-NOV-1999 (TREMBREL, 01; last sequence update)
DE	01-MAR-2001 (TREMBREL, 16; last annotation update)	DE	01-MAY-2000 (TREMBREL, 13; last annotation update)
DR	VPR PROTEIN (FRAGMENT).	DR	VPR PROTEIN.
VR		VR	
OS	Human immunodeficiency virus type 1.	OS	Human immunodeficiency virus type 1.
OT	Virus; Retrovirus; Lentivirus; Lentiviridae.	OT	Virus; Retrovirus; Lentivirus; Lentiviridae.
OX	NCBITAXID:11676;	OX	NCBITAXID:11676;
RN	[1]	RN	[1]
RP	SEQUENCE FROM N.A.	RP	SEQUENCE FROM N.A.
RA	STRAIN: INFANT FATE, A.	RA	STRAIN: INFANT, 04/57, H-MOSCOW, GERMAN
RK	Yedavalli V.R.; Cheppay G.; Ahmad N.;	RK	Fabre L.; Gotoh S.; Hori T.; Kondo T.; Hartmann S.; Gibbs J.
RT	Maintenance of an intact human immunodeficiency virus genome after one	RT	Goudsmit J.; J. Gen. Virol., 60:0-01996;
RL	following mother-to-infant transmission.	RL	EML; ZB857; CA92881.1;
IR	J. VIROL., 72:6337-6343 (1998).	IR	EMBL; EMBL; ITR-001.2;
DR	EMBL; AAF42894; AAC41064.1;	DR	PRIM; PR00522; VPR; 1;
DR	INTERPRO; IPR00012;	DR	PRIM; PR00522; VPR; 1;
DR	PIR; PIR00522; VPR; 1;	DR	PRIM; PR00522; VPR; 1;
DR	PRINTS; PR00444; HIVVPRPX;	DR	PRIM; PR00522; VPR; 1;
FT	NON-TER 67 AA;	FT	SEQUENCE: 67 AA; 7933 MW; 5281B9611B4750E CRC64;
QQ	SEQUENCE: 67 AA; 7933 MW; 5281B9611B4750E CRC64;	QQ	SEQUENCE: 67 AA; 7933 MW; 5281B9611B4750E CRC64;
Query Match	95.0%	Query Match	95.0%
Best Local Similarity	100.0%	Best Local Similarity	100.0%
Matches	19;	Matches	19;
Conservative	0;	Conservative	0;
Mismatches	0;	Mismatches	0;
Indels	0;	Indels	0;
Gaps	0;	Gaps	0;
Sequence From N.A.		Sequence From N.A.	
RESULT	7	RESULT	8
ID	Q9Q6G7	ID	Q79253
AC	Q9Q6G7;	AC	Q79253;
DT	01-MAY-2000 (TREMBREL, 13; created)	DT	01-MAY-1996 (TREMBREL, 01; created)
DT	01-MAY-2000 (TREMBREL, 13; last sequence update)	DT	01-MAY-1996 (TREMBREL, 01; last sequence update)
DI	01-MAR-2001 (TREMBREL, 16; last annotation update)	DI	01-MAY-2000 (TREMBREL, 13; last annotation update)
DR	TREMBREL	DR	VPR PROTEIN.
VR		VR	
OS	Human immunodeficiency virus type 1.	OS	Human immunodeficiency virus type 1.
OT	Virus; Retrovirus; Lentivirus; Lentiviridae.	OT	Virus; Retrovirus; Lentivirus; Lentiviridae.
OX	NCBITAXID:11676;	OX	NCBITAXID:11676;
RN	[1]	RN	[1]
RP	SEQUENCE FROM N.A.	RP	SEQUENCE FROM N.A.
RA	STRAIN:990407;	RA	STRAIN:990407;
RA	Anderson J.P.; Rodriguez A.G.; Learn G.H.; Madan A.; Malathyur C.;	RA	Anderson J.P.; Rodriguez A.G.; Learn G.H.; Madan A.; Malathyur C.;
RA	Coon M.; Girard M.; Ostrovsky S.; Hood L.; Mullins J.I.;	RA	Coon M.; Girard M.; Ostrovsky S.; Hood L.; Mullins J.I.;
RT	"Testing the hypothesis of a recombinant origin of human immunodeficiency virus type 1 lacking the 'm' subunit (part 2)" to the EMBL/Genbank/DBJ databases.	RT	"Testing the hypothesis of a recombinant origin of human immunodeficiency virus type 1 lacking the 'm' subunit (part 2)" to the EMBL/Genbank/DBJ databases.
RT	Submitted (part 2) to the EMBL/Genbank/DBJ databases.	RT	Submitted (part 2) to the EMBL/Genbank/DBJ databases.
RI	EMBL; AAF19734; AAC124386.1;	RI	EMBL; AAF19734; AAC124386.1;
DR	INTERPRO; IPR00012;	DR	INTERPRO; IPR00012;
DR	PRINTS; PR00522; VPR; 1;	DR	PRINTS; PR00522; VPR; 1;
DR	PRIM; PR00444; HIVVPRPX;	DR	PRIM; PR00444; HIVVPRPX;
DR	PRINTS; PR00444; HIVVPRPX;	DR	PRIM; PR00444; HIVVPRPX;
QQ	SEQUENCE: 93 AA; 1151 MW; 8429E8262AECB CRC64;	QQ	SEQUENCE: 94 AA; 11384 MW; 6093A809C9ED3 CRC64;
Query Match	95.0%	Query Match	95.0%
Best Local Similarity	100.0%	Best Local Similarity	100.0%
Matches	19;	Matches	19;
Conservative	0;	Conservative	0;
Mismatches	0;	Mismatches	0;
Indels	0;	Indels	0;
Gaps	0;	Gaps	0;
Sequence From N.A.		Sequence From N.A.	
RESULT	9	RESULT	9
ID	P88158	ID	P88158
AC	P88158;	AC	P88158;
DT	01-MAY-1997 (TREMBREL, 03; created)	DT	01-MAY-1997 (TREMBREL, 03; created)
DT	01-MAY-1997 (TREMBREL, 03; last sequence update)	DT	01-MAY-2000 (TREMBREL, 13; last sequence update)
DE	VPR PROTEIN.	DE	VPR PROTEIN.
GN		GN	
OS	Human immunodeficiency virus type 1.	OS	Human immunodeficiency virus type 1.
OT	Virus; Retrovirus; Lentivirus; Lentiviridae.	OT	Virus; Retrovirus; Lentivirus; Lentiviridae.
OX	NCBITAXID:11676;	OX	NCBITAXID:11676;
RN	[1]	RN	[1]
RP	SEQUENCE FROM N.A.	RP	SEQUENCE FROM N.A.
RA	Gao F.; Robertson D.L.; Morrison S.G.; Hui H.; Craig S.; Fultz P.N.;	RA	Gao F.; Robertson D.L.; Morrison S.G.; Hui H.; Craig S.; Fultz P.N.;
RA	Heger J.; Gralinski M.; Shaw G.M.; Hahn B.H.; Sharp P.M.;	RA	Heger J.; Gralinski M.; Shaw G.M.; Hahn B.H.; Sharp P.M.;
RA	Robertson D.L.; Morrison S.G.; Hui H.; Craig S.; Fultz P.N.;	RA	Robertson D.L.; Morrison S.G.; Hui H.; Craig S.; Fultz P.N.;
RA	Heger J.; Gralinski M.; Shaw G.M.; Hahn B.H.; Sharp P.M.;	RA	Heger J.; Gralinski M.; Shaw G.M.; Hahn B.H.; Sharp P.M.;
RA	Shuttle T.; Girard M.; Shaw G.M.; Hahn B.H.; Sharp P.M.;	RA	Shuttle T.; Girard M.; Shaw G.M.; Hahn B.H.; Sharp P.M.;
RA	Subunit "m" (part 2) to the EMBL/Genbank/DBJ databases.	RA	Subunit "m" (part 2) to the EMBL/Genbank/DBJ databases.
RI	EMBL; AAF19734; AAC124386.1;	RI	EMBL; AAF19734; AAC124386.1;
DR	INTERPRO; IPR00012;	DR	INTERPRO; IPR00012;
DR	PRINTS; PR00522; VPR; 1;	DR	PRINTS; PR00522; VPR; 1;
DR	PRIM; PR00444; HIVVPRPX;	DR	PRIM; PR00444; HIVVPRPX;
DR	PRINTS; PR00444; HIVVPRPX;	DR	PRIM; PR00444; HIVVPRPX;
QQ	SEQUENCE: 94 AA; 11384 MW; 6093A809C9ED3 CRC64;	QQ	SEQUENCE: 94 AA; 11384 MW; 6093A809C9ED3 CRC64;
Query Match	95.0%	Query Match	95.0%
Best Local Similarity	100.0%	Best Local Similarity	100.0%
Matches	19;	Matches	19;
Conservative	0;	Conservative	0;
Mismatches	0;	Mismatches	0;
Indels	0;	Indels	0;
Gaps	0;	Gaps	0;
Sequence From N.A.		Sequence From N.A.	







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Title: US-09-485-421-1\_CNPV\_59\_84  
Perfect score: 26  
Sequence: 1 ALTRI1QD1P1HRT3P8HPIGT 26

Scoring table:  
OTGO  
Gator 60 60 Gator 60 60

Searched: 412676 serials. 6065248A record.

word size : 0

Total number of hits satisfying chosen parameters: 412676

Maximum DB Seq length: 0  
Minimum DB Seq length: 0  
Maximum DB seq length: 200000000

**Post-processing:** Listing first 45 summaries

Database : A\_Geneseq\_0601;\*

卷之三

5. *Actias luna* (Linnaeus) 1758  
6. *Actias luna* (Linnaeus) 1758

Variables	Mean	SD
Persons per household	3.0	1.0
Persons per family	2.5	1.8
Persons per household per capita	1.8	0.4

12: <http://www.ncbi.nlm.nih.gov/pmc/articles/PMC2125889/>  
13: <http://www.ncbi.nlm.nih.gov/pmc/articles/PMC2125889/>

卷之三

JOURNAL OF CLIMATE

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pred. No. is the number of results predicted greater than or equal to the score

and is derived by analysis of the totality of the data.

SUMMARY

No.	Score	Match length	DB	ID
-----	-------	--------------	----	----

AAW9915  
AAW9916  
AAW9917

75 226 100.0 96 20 AAW99819  
76 300 0 96 20 AAW99818

8	26	96.3	96.70	AABV19820
9	23	88.5	96.	AABV198301
10	23	88.5	96.	AABV198304
11	23	84.5	49	AABV1068?







PS Claim 41; Fig 17; 131pp; English.  
XX  
XX The present invention provides the protein and genetic sequences for a  
XX number of known immunodominant regions (HRV) type 1, genotype B  
XX isolates. The sequences shown include the near full-length coding  
XX sequences from each isolate, and the poly-AUT, gtf, gtf, spf, spf, qaq, tat,  
XX rev and nef proteins. These can be used to detect the presence of HIV-1  
XX (uABR-) DAB RES FOUND.  
XX  
XX Hahn BH, Shaw GM, Gao F;  
XX  
XX These antibodies can be used in vaccines to prevent and treat HIV  
XX infection.

The present invention provides the protein and coding sequences of novel deoxyribonucleic acids of non-subtype B human immunodeficiency virus type I useful for detecting and isolating AIDS viruses and specific nucleotide sequence claim 41; Fig 17; 131pp; English.

isolates, the sequences shown include the most full-length coding sequences from each isolate, and the env, pol, gag, rev, env, gag, tat, rev and nef proteins. These can be used to detect the presence of HIV-1 in a sample and to produce antibodies against non-specified HIV-1 virus. These antibodies can be used in vaccines to prevent and treat HIV infection.

Query Match: 88.5%, score 23, DB 21, Length: 36,  
 Best Local Similarity: 100.0%, Pred No.: 7, 40, 160  
 Matches: 25, Cons. Purity: 0, Misalignments: 1, Total: 25

Qy	3	IRIQQIPIHFRIGCRHSRIGI	25
Db	61	irilqqltihririgerhsrii	83

11 AAB69304 Standard; Protel II; 96 AA.

200-AIR-2001 (first entry)

HYDROLOGIC AND HYDRAULIC ASPECTS OF THE RIVER TIDWELL

Human immunodeficiency virus type 1.

W0200026416-A1.

11 MAY 2000.

02 - NAV - 140000

(UABR-) UAB RES FOUND.

WPT : 2009-445631/31

RECENTLY, THE U.S. FOOD AND DRUG ADMINISTRATION APPROVED A PROTEIN-SPECIFIC MONOCLONAL ANTIBODY FOR TREATMENT OF AIDS. THIS APPROVAL IS BASED ON INDIVIDUAL PATIENTS' THERAPEUTIC RESPONSES TO THE MONOCLONAL ANTIBODY.

on investigation into viral particles. Vir induced cell cycle arrest, and cyclin kinase and cyclin-dependent kinases (cdk) is used to establish cell or animal models to study the pathogenicity of vpr, or structural analysis of vpr and its domains, for in vitro assembly of new sequences. For those that apply, in vitro or in vivo, for complementing the function of Vpr-like mutants in cell cultures, and to reduce toxicity of vpr induced by the N-terminal domain (signature (D), are soluble in water and can be formulated as highly concentrated solutions (molar), without protein denaturation, so are well suited to analysis by nuclear magnetic resonance X-ray or circular dichroism techniques. (D) adopt a folded structure, have biological activity comparable to that of viral Vpr, and can be produced in high purity on the milligram scale. This sequence represents the synthetic HIV 1 derived Vpr peptide SVPR48, (b), which is used in the method of the invention.

Sequence 49 AA;

query Match

Best local Similarity 100.0%; Pidx. No. 4; Sp. 1b; Length 49;

Matches 22; Conservat 0%; Mismatches 0%; Index 0%; Gaps 0%;

Query 3 IRILQWLFHGRGRISRG 24

Db 61 irilqlqflfhgrgrisrg 82

RESULT 14

AAR94544 Score 84.6%; Score 2.2%; DR 15; Length 96;

Matches 22; Conservat 0%; Mismatches 0%; Index 0%; Gaps 0%;

Query 3 IRILQWLFHGRGRISRG 24

Db 61 irilqlqflfhgrgrisrg 82

RESULT 15

AAR94544 Score 84.6%; Score 2.2%; DR 15; Length 96;

Matches 22; Conservat 0%; Mismatches 0%; Index 0%; Gaps 0%;

Query 3 IRILQWLFHGRGRISRG 24

Db 61 irilqlqflfhgrgrisrg 82

RESULT 16

AAR94544 Score 84.6%; Score 2.2%; DR 15; Length 96;

Matches 22; Conservat 0%; Mismatches 0%; Index 0%; Gaps 0%;

Query 3 IRILQWLFHGRGRISRG 24

Db 61 irilqlqflfhgrgrisrg 82

RESULT 17

AAR94544 Score 84.6%; Score 2.2%; DR 15; Length 96;

Matches 22; Conservat 0%; Mismatches 0%; Index 0%; Gaps 0%;

Query 3 IRILQWLFHGRGRISRG 24

Db 61 irilqlqflfhgrgrisrg 82

RESULT 18

AAR94544 Score 84.6%; Score 2.2%; DR 15; Length 96;

Matches 22; Conservat 0%; Mismatches 0%; Index 0%; Gaps 0%;

Query 3 IRILQWLFHGRGRISRG 24

Db 61 irilqlqflfhgrgrisrg 82

RESULT 19

AAR94544 Score 84.6%; Score 2.2%; DR 15; Length 96;

Matches 22; Conservat 0%; Mismatches 0%; Index 0%; Gaps 0%;

Query 3 IRILQWLFHGRGRISRG 24

Db 61 irilqlqflfhgrgrisrg 82

RESULT 20

AAR94544 Score 84.6%; Score 2.2%; DR 15; Length 96;

Matches 22; Conservat 0%; Mismatches 0%; Index 0%; Gaps 0%;

Query 3 IRILQWLFHGRGRISRG 24

Db 61 irilqlqflfhgrgrisrg 82

RESULT 21

AAR94544 Score 84.6%; Score 2.2%; DR 15; Length 96;

Matches 22; Conservat 0%; Mismatches 0%; Index 0%; Gaps 0%;

Query 3 IRILQWLFHGRGRISRG 24

Db 61 irilqlqflfhgrgrisrg 82

RESULT 22

AAR94544 Score 84.6%; Score 2.2%; DR 15; Length 96;

Matches 22; Conservat 0%; Mismatches 0%; Index 0%; Gaps 0%;

Query 3 IRILQWLFHGRGRISRG 24

Db 61 irilqlqflfhgrgrisrg 82

RESULT 23

AAR94544 Score 84.6%; Score 2.2%; DR 15; Length 96;

Matches 22; Conservat 0%; Mismatches 0%; Index 0%; Gaps 0%;

Query 3 IRILQWLFHGRGRISRG 24

Db 61 irilqlqflfhgrgrisrg 82

RESULT 24

AAR94544 Score 84.6%; Score 2.2%; DR 15; Length 96;

Matches 22; Conservat 0%; Mismatches 0%; Index 0%; Gaps 0%;

Query 3 IRILQWLFHGRGRISRG 24

Db 61 irilqlqflfhgrgrisrg 82

RESULT 25

AAR94544 Score 84.6%; Score 2.2%; DR 15; Length 96;

Matches 22; Conservat 0%; Mismatches 0%; Index 0%; Gaps 0%;

Query 3 IRILQWLFHGRGRISRG 24

Db 61 irilqlqflfhgrgrisrg 82

RESULT 26

AAR94544 Score 84.6%; Score 2.2%; DR 15; Length 96;

Matches 22; Conservat 0%; Mismatches 0%; Index 0%; Gaps 0%;

Query 3 IRILQWLFHGRGRISRG 24

Db 61 irilqlqflfhgrgrisrg 82

RESULT 27

AAR94544 Score 84.6%; Score 2.2%; DR 15; Length 96;

Matches 22; Conservat 0%; Mismatches 0%; Index 0%; Gaps 0%;

Query 3 IRILQWLFHGRGRISRG 24

Db 61 irilqlqflfhgrgrisrg 82

RESULT 28

AAR94544 Score 84.6%; Score 2.2%; DR 15; Length 96;

Matches 22; Conservat 0%; Mismatches 0%; Index 0%; Gaps 0%;

Query 3 IRILQWLFHGRGRISRG 24

Db 61 irilqlqflfhgrgrisrg 82

RESULT 29

AAR94544 Score 84.6%; Score 2.2%; DR 15; Length 96;

Matches 22; Conservat 0%; Mismatches 0%; Index 0%; Gaps 0%;

Query 3 IRILQWLFHGRGRISRG 24

Db 61 irilqlqflfhgrgrisrg 82

RESULT 30

AAR94544 Score 84.6%; Score 2.2%; DR 15; Length 96;

Matches 22; Conservat 0%; Mismatches 0%; Index 0%; Gaps 0%;

Query 3 IRILQWLFHGRGRISRG 24

Db 61 irilqlqflfhgrgrisrg 82

RESULT 31

AAR94544 Score 84.6%; Score 2.2%; DR 15; Length 96;

Matches 22; Conservat 0%; Mismatches 0%; Index 0%; Gaps 0%;

Query 3 IRILQWLFHGRGRISRG 24

Db 61 irilqlqflfhgrgrisrg 82

RESULT 32

AAR94544 Score 84.6%; Score 2.2%; DR 15; Length 96;

Matches 22; Conservat 0%; Mismatches 0%; Index 0%; Gaps 0%;

Query 3 IRILQWLFHGRGRISRG 24

Db 61 irilqlqflfhgrgrisrg 82

RESULT 33

AAR94544 Score 84.6%; Score 2.2%; DR 15; Length 96;

Matches 22; Conservat 0%; Mismatches 0%; Index 0%; Gaps 0%;

Query 3 IRILQWLFHGRGRISRG 24

Db 61 irilqlqflfhgrgrisrg 82

RESULT 34

AAR94544 Score 84.6%; Score 2.2%; DR 15; Length 96;

Matches 22; Conservat 0%; Mismatches 0%; Index 0%; Gaps 0%;

Query 3 IRILQWLFHGRGRISRG 24

Db 61 irilqlqflfhgrgrisrg 82

RESULT 35

AAR94544 Score 84.6%; Score 2.2%; DR 15; Length 96;

Matches 22; Conservat 0%; Mismatches 0%; Index 0%; Gaps 0%;

Query 3 IRILQWLFHGRGRISRG 24

Db 61 irilqlqflfhgrgrisrg 82

RESULT 36

AAR94544 Score 84.6%; Score 2.2%; DR 15; Length 96;

Matches 22; Conservat 0%; Mismatches 0%; Index 0%; Gaps 0%;

Query 3 IRILQWLFHGRGRISRG 24

Db 61 irilqlqflfhgrgrisrg 82

RESULT 37

AAR94544 Score 84.6%; Score 2.2%; DR 15; Length 96;

Matches 22; Conservat 0%; Mismatches 0%; Index 0%; Gaps 0%;

Query 3 IRILQWLFHGRGRISRG 24

Db 61 irilqlqflfhgrgrisrg 82

RESULT 38

AAR94544 Score 84.6%; Score 2.2%; DR 15; Length 96;

Matches 22; Conservat 0%; Mismatches 0%; Index 0%; Gaps 0%;

Query 3 IRILQWLFHGRGRISRG 24

Db 61 irilqlqflfhgrgrisrg 82

RESULT 39

AAR94544 Score 84.6%; Score 2.2%; DR 15; Length 96;

Matches 22; Conservat 0%; Mismatches 0%; Index 0%; Gaps 0%;

Query 3 IRILQWLFHGRGRISRG 24

Db 61 irilqlqflfhgrgrisrg 82

RESULT 40

AAR94544 Score 84.6%; Score 2.2%; DR 15; Length 96;

Matches 22; Conservat 0%; Mismatches 0%; Index 0%; Gaps 0%;

Query 3 IRILQWLFHGRGRISRG 24

Db 61 irilqlqflfhgrgrisrg 82

RESULT 41

AAR94544 Score 84.6%; Score 2.2%; DR 15; Length 96;

Matches 22; Conservat 0%; Mismatches 0%; Index 0%; Gaps 0%;

Query 3 IRILQWLFHGRGRISRG 24

Db 61 irilqlqflfhgrgrisrg 82

RESULT 42

AAR94544 Score 84.6%; Score 2.2%; DR 15; Length 96;

Matches 22; Conservat 0%; Mismatches 0%; Index 0%; Gaps 0%;

Query 3 IRILQWLFHGRGRISRG 24

Db 61 irilqlqflfhgrgrisrg 82

RESULT 43

AAR94544 Score 84.6%; Score 2.2%; DR 15; Length 96;

Matches 22; Conservat 0%; Mismatches 0%; Index 0%; Gaps 0%;

Query 3 IRILQWLFHGRGRISRG 24

Db 61 irilqlqflfhgrgrisrg 82

RESULT 44

AAR94544 Score 84.6%; Score 2.2%; DR 15; Length 96;

Matches 22; Conservat 0%; Mismatches 0%; Index 0%; Gaps 0%;

Query 3 IRILQWLFHGRGRISRG 24

Db 61 irilqlqflfhgrgrisrg 82

RESULT 45

AAR94544 Score 84.6%; Score 2.2%; DR 15; Length 96;

Matches 22; Conservat 0%; Mismatches 0%; Index 0%; Gaps 0%;

Query 3 IRILQWLFHGRGRISRG 24

Db 61 irilqlqflfhgrgrisrg 82

RESULT 46

AAR94544 Score 84.6%; Score 2.2%; DR 15; Length 96;

Matches 22; Conservat 0%; Mismatches 0%; Index 0%; Gaps 0%;

Query 3 IRILQWLFHGRGRISRG 24

Db 61 irilqlqflfhgrgrisrg 82

RESULT 47

AAR94544 Score 84.6%; Score 2.2%; DR 15; Length 96;

Matches 22; Conservat 0%; Mismatches 0%; Index 0%; Gaps 0%;

Query 3 IRILQWLFHGRGRISRG 24

Db 61 irilqlqflfhgrgrisrg 82

RESULT 48

AAR94544 Score 84.6%; Score 2.2%; DR 15; Length 96;

Matches 22; Conservat 0%; Mismatches 0%; Index 0%; Gaps 0%;

Query 3 IRILQWLFHGRGRISRG 24

Db 61 irilqlqflfhgrgrisrg 82

RESULT 49

AAR94544 Score 84.6%; Score 2.2%; DR 15; Length 96;

Matches 22; Conservat 0%; Mismatches 0%; Index 0%; Gaps 0%;

Query 3 IRILQWLFHGRGRISRG 24

Db 61 irilqlqflfhgrgrisrg 82

RESULT 50

AAR94544 Score 84.6%; Score 2.2%; DR 15; Length 96;

Matches 22; Conservat 0%; Mismatches 0%; Index 0%; Gaps 0%;

Query 3 IRILQWLFHGRGRISRG 24

Db 61 irilqlqflfhgrgrisrg 82

RESULT 51

AAR94544 Score 84.6%; Score 2.2%; DR 15; Length 96;

Matches 22; Conservat 0%; Mismatches 0%; Index 0%; Gaps 0%;

Query 3 IRILQWLFHGRGRISRG 24

Db 61 irilqlqflfhgrgrisrg 82

RESULT 52

AAR94544 Score 84.6%; Score 2.2%; DR 15; Length 96;

Matches 22; Conservat 0%; Mismatches 0%; Index 0%; Gaps 0%;

Query 3 IRILQWLFHGRGRISRG 24

Db 61 irilqlqflfhgrgrisrg 82

RESULT 53

AAR94544 Score 84.6%; Score 2.2%; DR 15; Length 96;

Matches 22; Conservat 0%; Mismatches 0%; Index 0%; Gaps 0%;

Query 3 IRILQWLFHGRGRISRG 24

Db 61 irilqlqflfhgrgrisrg 82

RESULT 54

AAR94544 Score 84.6%; Score 2.2%; DR 15; Length 96;

Matches 22; Conservat 0%; Mismatches 0%; Index 0%; Gaps 0%;

Query 3 IRILQWLFHGRGRISRG 24

Db 61 irilqlqflfhgrgrisrg 82

Best local similarity 100.0%; Pred. No. 7, 2e-15; Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

NAB10685  
11D AAB10685 standard; peptide: 96 AA.  
XX  
AC AAB10685;  
XX

RESULT 14  
AAW5304G  
ID AAW5304G standard; Peptide: 96 AA.  
XX  
AC AAW5304G;  
XX  
DT 17-JUL-1998 (first entry)  
XX  
DF HIV-1 polypeptide.  
XX

Recombinant plant virus; HIV-1; protein production; immunisation; fusion derived protein; simian immunodeficiency virus; Tat protein; rhabdovirus.

Human immunodeficiency virus type 1

PN WO9808375 A1.

XX

05-MAR-1999.

PT

XX

DE

XX

Wed Oct 3 13:40:08 2001

115-09-485-421-1 copy 59 84 rag

Page 8

108

Scallop suspension cost per kg, 2001, £14.25 (2001)

"M" protein = protein selected using sw model

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Title: US\_09-485-421-1\_COPY\_17\_36  
Report score: 20  
Sequence: I.TWILLELEELLEKNEAVWHEPR

Scoring table: oligo Gapper 60.0 , gapext 60.0

Searched: 94435 Seqs, 3425486 residues

Word size: 10

Total number of hits satisfying chosen parameters: 94435

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: listing first 45 summaries

Database: SWISSPROT\_39 \*

Pred. No. is the number of results predicted by chance, i.e. how a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

#### ALIGNMENTS

RESULT	1
ID	VPR_HV1B1
TI	VPR_HV1B1 STANDARD
AC	PU5926; Q85577;
DT	01-NOV-1988 (Rel.: 09, Last sequence update)
DI	01-NOV-1988 (Rel.: 09, Last sequence update)
DT	15-JUL-1998 (Rel.: 06, Last affiliation update)
DE	VPR PROTEIN (RDP PROTEIN).
GN	VPR.
GG	Human immunodeficiency virus type 1 (RH10 isolate) (HIV-1), Human immunodeficiency virus type 1 (HXB2 isolate) (HIV-1), Human immunodeficiency virus type 1 (clone 1) (HIV-1), Human immunodeficiency virus type 1 (HXB3 isolate) (HIV-1), Human immunodeficiency virus type 1 (clone 2) (HIV-1), Human immunodeficiency virus type 1 (HXB2 isolate) (HIV-1).
OS	Virus; Retrovirus; retroviridae; Lentiviridae.
OC	Virus; Retrovirus; retroviridae; Lentiviridae.
NR	NCBI_TaxID:1167, 11705, 11707, 11709, 11700; 111
RN	SEQUENCE FROM N.A.
RC	STRAIN ISOLATE_BA10;
RX	MLINE_8511123; PubMed=2578615;
RA	Falter L., Haschke W., Patavina P., Livak K.L., Staretch B.R., Jost-Lyon S.F., Tschudin R., Patavina P., Whitehorn B.A., Bartholomaeus M., Tschudin J.A., Whitehorn B.A., Tautenberger J.A., Papas T.S., Ghayeb J., Chantel N.T., Gallo R.C., Wond-Staal F.J.,
RA	"Complete nucleotide sequence of the AIDS virus, HIV-111," NATURE 213:277-284(1985).
RA	SHIMURA FROM H.A.
RC	SPAIN-1 ISOLATE_HV1B2;
RX	PMID:87299196; PubMed=3004055;
RA	Palter L., Fisher A., Jagodinski J.L., Matsuya H., Lion R., S., Gallo R.C., Wong-Staal F.J.
RT	"Complete nucleotide sequences of functional clones of the AIDS virus," J. Virol. 61:5115-5116 (1987).
RT	AIDS PAT. HUM. RETROVIRUSES 2:57-63 (1987).
RN	131
RC	SEQUENCE FROM N.A.
RX	MLINE_8511123; PubMed=2578615;
RA	Shaw G.M., Gallo R.C., Gordon N., Crowley R., Schaber M., Kramer P., Wond-Staal F.J.,
RA	"HIV-111 one gene products synthesised in E. coli are recognised by antibodies present in the sera of AIDS patients," NATURE 314:579-580(1985).
RT	"Antibodies from the sera of AIDS patients recognise novel proteins of human T-lymphotropic virus type III: immune reactivity of the T products with sera from acquired immune deficiency syndrome patients," Proc. Natl. Acad. Sci. U.S.A. 83:2203-2213(1986).
RN	151
RP	SEQUENCE FROM N.A.
RC	STRAIN ISOLATE_PV2;







AC P05952;  
 DT 31-Nov-1988 (Rel. 39, Created)  
 OR 01-Nov-1988 (Rel. 39, Last sequence update)  
 CC  
 OC  
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 entities requires a license agreement (see <http://www.ist-sid.ch/announce/>).  
 CC or send an email to license@ist-sid.ch.  
 CC  
 CC  
 CC  
 DR FMDU: M17451; AAA45155; 1;  
 DR HIV; M17451; AAA45155; 1;  
 DR HIV; M17451; AAA45155; 1;  
 DR HIV; M17451; AAA45155; 1;  
 DR Ptang; PF00522; VPR; 1;  
 DR PRNTS; PR00444; HIVWPVX;  
 KW AIDS;  
 KW Sequence; 97 AA.; 1155 MW; 85BC4E4959BA44 CRC64;  
 SQ

Query Match 50.0%; Score 10; DB 1; Length 96;  
 Best local similarity 100.0%; Pred. No. 0; 0/24; Mismatches 0; Indels 0; Gaps 0;  
 Matches 13; Conservative 0; MisMatches 0; InDelS 0;

OY 2 WILEELIEK 11  
 11111111  
 Db 18 WILEELIEK 27

RESULT 11  
 VPR\_HV1Y2; STANDARD; PRT; 96 AA.  
 AC P12519;  
 DT 01-OCT-1986 (Rel. 12, Created)  
 DT 01-OCT-1989 (Rel. 12, last sequence update)  
 LE VPR PROTEIN (R ORF PROTEIN).  
 GN  
 OS Human immunodeficiency virus type 1 (222CUG-234 isolate) (HIV-1).  
 OC Viruses; Retroviridae; Lentiviridae  
 OX NCBI\_TAXID: 11583;  
 RN [1]  
 RP Sequence FROM N.A.  
 KA Theodore T., Buckler White A.;  
 RL Submitted (Nov 1988) to the HIV data bank.

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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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 CC entities requires a license agreement (see <http://www.ist-sid.ch/announce/>).  
 CC or send an email to license@ist-sid.ch.  
 CC  
 DR EMBL; K02007; AAC66978; 1;  
 DR HIV; K02007; VPRSE2;  
 DR InterPro; IPB01012; -;  
 DR Ptang; PF00522; VPR; 1;  
 DR PRNTS; PR00444; HIVWPVX;  
 KW AIDS;  
 KW Sequence; 97 AA.; 1155 MW; 491949E2A932430 CRC64;  
 SQ

Query Match 50.0%; Score 10; DB 1; Length 97;  
 Best local similarity 100.0%; Pred. No. 0; 0/24; Mismatches 0; Indels 0; Gaps 0;  
 Matches 10; Conservative 0; MisMatches 0; InDelS 0;

OY 2 WILEELIEK 11  
 11111111  
 Db 18 WILEELIEK 27

RESULT 13  
 VPR\_HV1Y2; STANDARD; PRT; 97 AA.  
 AC P35957;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, last sequence update)  
 LE VPR PROTEIN (R ORF PROTEIN).  
 GN  
 OS Human immunodeficiency virus type 1 (YU-2 isolate) (HIV-1).  
 OC Viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TAXID: 36377;  
 RN [1]  
 RP Sequence FROM N.A.  
 RK MEDLINE-93021487; PubMed 1404605;  
 RA Li Y., Hui H., Burgess C.J., Price R.W., Sharp P.M., Hahn B.H.,  
 RA Shaw G.M.;  
 RT "Complete nucleotide sequence, deduced organization, and biological  
 RT properties of the human immunodeficiency virus type 1 genome, including  
 RT limited infectiveness and complementation";  
 RL J. Virol. 66:6597-6606(1992).

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 modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (see <http://www.ist-sid.ch/announce/>).

OY 2 WILEELIEK 11  
 11111111  
 It 18 WILEELIEK 27

RESUL 12  
 VPR\_HV1A2  
 ID VPR\_HV1A2 STABILITY: PRT; 97 AA.



Gencore version 4.5  
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AM protein = protein search, using sw mode!

ket on: October 3, 2001, 13:25:46 ; search time 18.81 Seconds  
(without alignments)

Scoring table: ORCA

Query 600 , capex+600

Searched: 197339 seqs., 20590346 residues

Word size : 0

total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0

Maximum DB seq length: 299999999

Post-processing: listing first 45 summaries

Database : Issued patents MA:\*

1: 1999-08-24T09:55:55Z P-EP \*

2: 1999-08-24T09:55:55Z P-EP \*

3: 1999-08-24T09:55:55Z P-EP \*

4: 1999-08-24T09:55:55Z P-EP \*

5: 1999-08-24T09:55:55Z P-EP \*

6: 1999-08-24T09:55:55Z P-EP \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score or the result being printed and is derived by analysing all the total score distribution.

### SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	2.1	9.1	46	2 US-09-485-421-1
2	2.2	84.6	9.6	3 US-09-485-421-1
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4	4.3	50.0	13	5 US-09-485-421-1
5	1.3	50.0	13	6 US-09-485-421-1
6	1.3	50.0	13	7 US-09-485-421-1
7	7.2	46.3	7.2	8 US-09-485-421-1
8	1.2	46.3	7.2	9 US-09-485-421-1
9	1.2	46.3	7.2	10 US-09-485-421-1
10	9.9	34.6	9	11 US-09-485-421-1
11	9	34.6	9	12 US-09-485-421-1
12	9	34.6	9	13 US-09-485-421-1
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25	6	23.1	254	26 US-09-485-421-1
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95	3	19.2	3	96 US-09-485-421-1
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98	3	19.2	3	99 US-09-485-421-1
99	3	19.2	3	100 US-09-485-421-1

### ALIGNMENTS

RESULT 1

US-09-301-915-1

Sequence 1, Application US-09-301-915-1

Patent No. 5861161

GENERAL INFORMATION:

APPLICANT: COHEN, Eric A.

APPLICANT: BERGERON, Dominique

ATTORNEY: MICHAILI, Florence

APPLICANT: YANG, Xian

APPLICANT: YOUNG, Karen

NAME OF INVENTOR: DAVID A. JACKSON

NUMBER OF SPECIESSES: 5

CORRESPONDENCE ADDRESS:

ADDRESS: 100 FAIRFIELD PLAZA, 411 HAKENBACH AVENUE

CITY: HAKENBACH

STATE: N.J.

COUNTY: U.S.A.

ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: MS-DOS

SOFTWARE: PatternIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

ATTL. ATTN: JON MEE,

FILED: 1998-03-19

FILING DATE: 1998-03-19

CLASSIFICATION: 536

ATTORNEY/PAINTER: THOMAS:

NAME: JACKSON, David A.

REGISTRATION NUMBER: 26,742

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-487-5800

FAX: 201-443-1684

TELEFAX: 1-33521

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 96 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

US-09-485-421-1

W. B. F. L. U. P. D. I. J. J. H. E. R. T. C. H. O. S. K. R. G. 24  
W. B. F. L. U. P. D. I. J. J. H. E. R. T. C. H. O. S. K. R. G. 24

AMMEESEE: KRAMER & JACKSON  
STREET: Continental Plaza, 411 Hackensack Avenue  
CITY: Hackensack  
STATE: N.J.

RE-5014 2  
05-08-704 8500 15  
S-photocopy. Application US-A19-204866  
patent No. 3,619,692  
GENERAL INSTRUMENT;  
AUSTRIANI; KOPROWSKI; Blatty  
AUSTRIANI; Wissotsky; Vichai  
AUSTRIANI; Blomquist; Baumgarten, C.  
AUSTRIANI; Modestka; Anton  
TITLE OF INVENTION: Photoelectric device with liquid violet  
LILIE-AP INVENTIVE COLOR Proteins

CONCERNED ADDRESS,  
AUSTIN-SCHILL, 1545, Louise Street, 14th Fl.,  
DETROIT, MI 48202-2000.  
TEL: (313) 961-1000.  
FAX: (313) 961-1001.  
E-MAIL: [ASCHILL@AOL.COM](mailto:ASCHILL@AOL.COM)

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (201) 487-5000  
TELEFAX: 201-343-1684  
TELEX: 134524  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 96 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: No  
BS-08-524-G4A-1

CLASSIFICATION  
ATTACHEMENT  
NAME: FRED A. LAMM  
REFUGEE NUMBER: 31-253  
REFERRED REFUGEE NUMBER: 319-0017  
REFUGEE IMMIGRATION INFORMATION:  
FREIGHTING: (211) 192-1040

INTRODUCTION: The following is a brief introduction to the "Shaw-Turkevich" method of synthesis of organic acids. It is intended for the use of students in the field of organic chemistry, particularly those interested in the synthesis of organic acids. The method is based on the use of a reagent, which is a mixture of two organic acids, namely, acetic acid and propionic acid. The reagent is used to synthesize a variety of organic acids, including carboxylic acids, aldehydes, ketones, and esters. The method is simple and can be easily carried out in the laboratory. The results are reliable and reproducible. The method is also suitable for the synthesis of organic acids in large quantities.

APPLICANT: KOROBITSY, PHILIPPE  
TITLE OF INVENTION: An Altered Major Histocompatibility  
Title of Invention: Complex (B1) Determinant and Methods for Using the  
Title of Invention: Determinant  
NUMBER OF SIGNATURES: 127  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fimegna, Henderson, Farabow, Garrett &  
STREET: 1300 I Street, N.W., Suite 700

Apprenticeship training is a key element of vocational training.

COMPUTER: DELL  
ZIP #: 29005-3415  
COMPUTER REASONABLE FORM:  
MEDIA TYPE: Floppy Disk  
COMPATIBILITY: IBM PC compatible

APPLICANT: BERNARD R. A.  
APPLICANT: BECKER, Dennis

1. NUMBER: IBM PC compat. rule  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Batch in Release #1.0, Version #1.2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: 155/1848905

APPLIANT, FUGA, KORNBERG, CITY  
TOWN OF INVENTION, PROTEIN, INC., HAWAII, VIRGIN ISLANDS, BASED

PATENT APPLICATION DATA:

APPLICATION NUMBER: US 07/801,818  
FILING DATE: 05-DEC-1991

CLASSIFICATION: 530  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/7792,473

FILING DATE: 15 NOV 1991

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Potter, Jane E. K.

REGISTRATION NUMBER: 33,342

REFERENCE NUMBER: C2465,345,010,0100

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-408-4400

TELEFAX: 202-408-4400

SEQUENCE CHARACTERISTICS:

LENGTH: 13 amino acids

TYPE: amino acid

TOPOLOGY: linear

LENGTH: 13 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US 08 481 983 B 58

Query Match: 50,087 Score: 13; DB 27 Length: 13;  
Best Local Similarity: 100,0%; Pred. No.: 1,20-07;  
Mat. No.: 13; Mismatches: 0; Index: 0;  
Cyg 10 LIPIDPROGRESS 22  
Db 1 LIPIDPROGRESS 13

RESULT: 6 US 08 470-476,58

Sequence 58, Application US/08470476

PATENT NO. 6,153,408

GENERAL INFORMATION:

APPLICANT: Bourcet, Estelle

APPLICANT: Abastado, Jean-Pierre

APPLICANT: Kourilsky, Philippe

TITLE OF INVENTION: Altered Major histocompatibility complex

NUMBER OF SEQUENCES: 148

CORRESPONDENCE ADDRESS:

ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &

ADDRESS: Duane, Morris, Aronson, Gassner, Armand

CITY: Washington

STATE: D.C.

ZIP: 20005-3315

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC DOS/MS-DOS

SOFTWARE: Paton's Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/370,476

FILING DATE: 07-JUN-1993

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/7792,473

FILING DATE: 15 NOV 1991

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Meyers, Kenneth J.

REGISTRATION NUMBER: 25,146

REFERENCE NUMBER: 03,345,010,0100

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-408-4400

TELEFAX: 202-408-4400

SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide

Query Match: 50,087 Score: 13; DB 27 Length: 13;  
Best Local Similarity: 100,0%; Pred. No.: 1,20-07;  
Mat. No.: 13; Mismatches: 0; Index: 0;  
Cyg 10 LIPIDPROGRESS 22  
Db 1 LIPIDPROGRESS 13

RESULT: 6 US 08 470-476,58

Sequence 58, Application US/08470476

PATENT NO. 6,153,408

GENERAL INFORMATION:

APPLICANT: Bourcet, Estelle

APPLICANT: Abastado, Jean-Pierre

APPLICANT: Kourilsky, Philippe

APPLICANT: Lohr, Yu-chun

APPLICANT: Ojus, David

APPLICANT: Castroue, Armand

TITLE OF INVENTION: Altered Major histocompatibility complex

NUMBER OF SEQUENCES: 127

CORRESPONDENCE ADDRESS:

ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &

ADDRESS: Duane, Morris, Aronson, Gassner, Armand

CITY: Washington

STATE: D.C.

ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC DOS/MS-DOS

SOFTWARE: Paton's Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/370,476

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/117,575

FILING DATE: 07-SEP-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/7792,787

FILING DATE: 15-NOV-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/801,818

FILING DATE: 07-JUN-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/7792,473

FILING DATE: 15 NOV 1991

ATTORNEY/AGENT INFORMATION:

NAME: Meyers, Kenneth J.

REGISTRATION NUMBER: 25,146

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-408-4400

TELEFAX: 202-408-4400

INFORMATION FOR SEQ ID NO: 58:

SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide

US-08-370-476-58



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; LENGTH: 78
; TYPE: PRI
; ORGANISM: Human; immunodeficiency virus type 1
; US-09-124,900,5

; QUERY MATCHES: 34,5%; Score: 9; DB 1; Length: 9;
; Best Local Similarity: 100.0%; Pred. No.: 1.5e+05;
; Matches: 9; Conservative: 0; Mismatches: 0; Indexes: 0; Gaps: 0;
; Query: 3 FRIGCRSHR 14
; Db: 61 FRIGCRSHR 72

; RESULT: 10
; US-07-841,662-30
; Sequence: 30, Application US-07841662
; Patent No.: 5,148,113
; GENERAL INFORMATION:
; APPLICANT: Peterson, Per A
; APPLICANT: Jackson, Michael
; APPLICANT: Lemalade-Demoyen, Pierre
; TITLE OF INVENTION: IN VITRO ACTIVATION OF CYTOTOXIC T CELLS
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute
; STREET: 10554 N. 5529921st Torrey Pines Road, TPC 5
; CITY: La Jolla
; STATE: California
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patcuitic Novellus #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; ATTORNEY/AGENT NUMBER: 92-111-2111
; FILING DATE: 10-MAR-1994
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/841,662
; FILING DATE: 19-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Logan, April
; REGISTRATION NUMBER: 33,950
; REFERENCE NUMBER: SPFU001P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 554-2937
; TELEFAX: (619) 554-6312
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: Single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; US-08-209-797-30

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 554-2937
; TELEFAX: (619) 554-6312
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: Single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; US-07-841,662-30

; Query Match: 34,6%; Score: 9; DB 1; Length: 9;
; Best Local Similarity: 100.0%; Pred. No.: 1.5e+05;
; Matches: 9; Conservative: 0; Mismatches: 0; Indexes: 0; Gaps: 0;
; Query: 14 FRIGCRSHR 22
; Db: 1 FRIGCRSHR 9

; RESULT: 12
; US-08-669,685-30
; Sequence: 30, Application US-08669685
; Patent No.: 5,827,37
; GENERAL INFORMATION:
; APPLICANT: Peterson, Per A
; APPLICANT: Jackson, Michael
; APPLICANT: Lemalade-Demoyen, Pierre
; TITLE OF INVENTION: IN VITRO ACTIVATION OF CYTOTOXIC T CELLS
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute
; STREET: 10556 No. 52277,7th floor, Pines Road, TPC 8
; CITY: La Jolla
; LENGTH: 78
; TYPE: PRI
; ORGANISM: Human; immunodeficiency virus type 1
; US-09-124,900,5

; QUERY MATCHES: 46,2%; Score: 12; DB 4; Length: 78;
; Best Local Similarity: 100.0%; Pred. No.: 5.0e+06;
; Matches: 12; Conservative: 9; Mismatches: 0; Indexes: 0; Gaps: 0;
; Query: 3 FRIGCRSHR 14
; Db: 61 FRIGCRSHR 72
; RESULT: 10
; US-07-841,662-30
; Sequence: 30, Application US-07841662
; Patent No.: 5,148,113
; GENERAL INFORMATION:
; APPLICANT: Peterson, Per A
; APPLICANT: Jackson, Michael
; APPLICANT: Lemalade-Demoyen, Pierre
; TITLE OF INVENTION: IN VITRO ACTIVATION OF CYTOTOXIC T CELLS
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute
; STREET: 10556 No. 52277,7th floor, Pines Road, TPC 8
; CITY: La Jolla
; LENGTH: 78
; TYPE: PRI
; ORGANISM: Human; immunodeficiency virus type 1
; US-09-124,900,5

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TOPOLogy: linear  
 MOLECULE TYPE: peptide  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 FRAGMENT TYPE: internal  
 US-09-039-982A 41

Search completed: October 3, 2001, 13:25:46  
 Job time: 124 sec

Query Match 34.6%; Score 9; DB 4; Length 9;  
 Best Local Similarity 100.0%; Prc. No. 1.5e+05;  
 Marches 4; Conservative 0; Mismatches 0;  
 Index 0; Gaps 0;

QY 14 FRIGCRHRS 22  
 Db 1 FRIGCRHRS 9

RESULT 15  
 US-09-039-641-41

; Sequence 41, Application US/09039641

; Patent No. 6251627

; GENERAL INFORMATION:

; APPLICANT: Cai, Zeiling

; APPLICANT: Sorenson, Jonathan

; APPLICANT: Brummark, Anders

; APPLICANT: Jackson, Michael

; APPLICANT: Peterson, Per A

; TITLE OF INVENTION ANTIGEN PRESENTING SYSTEM AND METHODS FOR

; TITLE OF INVENTION ACTIVATION OF T-CELLS

; NUMBER OF SEQUENCES: 45

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: OLSON & HIERL, Ltd.

; STREET: 20 No. F-251627th Wacker Drive, Suite 3000

; CITY: Chicago

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60606

; COMPUTER READABLE FORM:

; MEDIUM TYPE: FLOPPY disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PATENT IN FILER-AS, #1.0, Version 1.0, 25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US-09-039-641

; FILING DATE: 8-MAR-1995

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Olson, Anne M.

; REGISTRATION NUMBER: 30,203

; REFERENCE/SEQUENCE NUMBER: TSR14710

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (312) 580-1180

; TELEFAX: (312) 580-1189

; INFORMATION FOR SEQ ID NO: 41:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 9 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; FRAGMENT TYPE: internal

; US-09-039-641-41

Query Match 34.6%; Score 9; DB 4; Length 9;  
 Best Local Similarity 100.0%; Prc. No. 1.5e+05;  
 Marches 4; Conservative 0; Mismatches 0;  
 Index 0; Gaps 0;

QY 14 FRIGCRHRS 22  
 Db 1 FRIGCRHRS 9

Db 1 FRIGCRHRS 9

Wed Oct 3 13:40:09 2001

us-09-485-421-1\_copy\_59\_84.rai







Q: Query Match Similarity: 23.1%; Score: 67; Length: 52;  
 Host Local Similarity: 100.0%; Pred.: No.; Mismatches: 0; Indels: 0; Gaps: 0;  
 Matches: 67; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;  
 A: Reference number: Reference: RBL0002; RBL0002; NID: 227354; P1DN: AAF42133.1; P1D: 9722734  
 A: Moltype: Preliminary  
 A: Residues: 1-52; P1L  
 A: Cross-references: 0; AAF42133.1; P1DN: AAF42133.1; P1D: 9722734  
 A: Name: RBL002

A: Name: RBL002

RESULT 15

S03067

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\*\*M\_Protein - protein search, using SW model  
 -> on: october 3, 2001, 14:40:12 : search time 13:32:56 (without alignments)  
 (without alignments)  
 103,204 million, 0.11 CPU, 8.59 sec  
 filter: 0S-09-485-421-1\_COPY\_59\_R4  
 Perfect score: 26  
 Sequence: 1 ALTRILOCUTIFERIGEPRVPGHSP11 26  
 Scoring table: Q115  
 Gapoff 60.0 , Gapext 6.0, 0  
 Total number of hits satisfying chosen parameters: 425026  
 Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000  
 Post-processing: listing first 45 summaries  
 Database : SPREMBL\_16,\*  
 1: sp-archaea;\*  
 2: sp-bacteria;\*  
 3: sp-fungi;\*  
 4: sp-human;\*  
 5: sp-invertebrates;\*  
 6: sp-mammal;\*  
 7: sp-mhc;\*  
 8: sp-mycobacter;\*  
 9: sp-phage;\*  
 10: sp-plant;\*  
 11: sp-rat;\*  
 12: sp-unclassified;\*  
 13: sp-vertebrate;\*  
 14: sp-virus;\*  
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

RESULT	SCORE	QUERY	MATCHES	DP	ID	DESCRIPTION
073399	96.00	96.14	073399	073399	073399	073399 human immunoglobulin heavy chain 1
1	26.00	96.14	073401	073401	073401	073401 human immunoglobulin heavy chain 1
2	25.99	96.14	073401	073401	073401	073401 human immunoglobulin heavy chain 1
3	26.00	96.14	073405	073405	073405	073405 human immunoglobulin heavy chain 1
4	26.00	96.14	073405	073405	073405	073405 human immunoglobulin heavy chain 1
5	26.00	96.14	073408	073408	073408	073408 human immunoglobulin heavy chain 1
6	26.00	96.14	073410	073410	073410	073410 human immunoglobulin heavy chain 1
7	26.00	96.14	073417	073417	073417	073417 human immunoglobulin heavy chain 1
8	26.00	96.14	073425	073425	073425	073425 human immunoglobulin heavy chain 1
9	26.00	96.14	073424	073424	073424	073424 human immunoglobulin heavy chain 1
10	26.00	96.14	073424	073424	073424	073424 human immunoglobulin heavy chain 1
11	26.00	96.14	073424	073424	073424	073424 human immunoglobulin heavy chain 1
12	26.00	96.14	073420	073420	073420	073420 human immunoglobulin heavy chain 1
13	26.00	96.14	073429	073429	073429	073429 human immunoglobulin heavy chain 1
14	26.00	96.14	073429	073429	073429	073429 human immunoglobulin heavy chain 1
15	25.99	95.14	073418	073418	073418	073418 human immunoglobulin heavy chain 1
16	25.99	95.14	073409	073409	073409	073409 human immunoglobulin heavy chain 1
17	25.99	95.14	073419	073419	073419	073419 human immunoglobulin heavy chain 1
18	25.99	95.14	073419	073419	073419	073419 human immunoglobulin heavy chain 1
19	25.99	95.14	073402	073402	073402	073402 human immunoglobulin heavy chain 1
20	25.99	95.14	073406	073406	073406	073406 human immunoglobulin heavy chain 1
21	25.99	95.14	073401	073401	073401	073401 human immunoglobulin heavy chain 1
22	25.99	95.14	073401	073401	073401	073401 human immunoglobulin heavy chain 1
23	25.99	95.14	073404	073404	073404	073404 human immunoglobulin heavy chain 1
24	25.99	95.14	073416	073416	073416	073416 human immunoglobulin heavy chain 1
25	25.99	95.14	073412	073412	073412	073412 human immunoglobulin heavy chain 1
26	25.99	95.14	073434	073434	073434	073434 human immunoglobulin heavy chain 1
27	25.99	95.14	073424	073424	073424	073424 human immunoglobulin heavy chain 1
28	25.99	95.14	073424	073424	073424	073424 human immunoglobulin heavy chain 1
29	25.99	95.14	073424	073424	073424	073424 human immunoglobulin heavy chain 1
30	25.99	95.14	073428	073428	073428	073428 human immunoglobulin heavy chain 1
31	25.99	95.14	073428	073428	073428	073428 human immunoglobulin heavy chain 1
32	25.99	95.14	073428	073428	073428	073428 human immunoglobulin heavy chain 1
33	25.99	95.14	073428	073428	073428	073428 human immunoglobulin heavy chain 1
34	25.99	95.14	073428	073428	073428	073428 human immunoglobulin heavy chain 1
35	25.99	95.14	073428	073428	073428	073428 human immunoglobulin heavy chain 1
36	25.99	95.14	073428	073428	073428	073428 human immunoglobulin heavy chain 1
37	25.99	95.14	073428	073428	073428	073428 human immunoglobulin heavy chain 1
38	25.99	95.14	073428	073428	073428	073428 human immunoglobulin heavy chain 1
39	25.99	95.14	073428	073428	073428	073428 human immunoglobulin heavy chain 1
40	25.99	95.14	073428	073428	073428	073428 human immunoglobulin heavy chain 1
41	25.99	95.14	073428	073428	073428	073428 human immunoglobulin heavy chain 1
42	25.99	95.14	073428	073428	073428	073428 human immunoglobulin heavy chain 1
43	25.99	95.14	073428	073428	073428	073428 human immunoglobulin heavy chain 1
44	25.99	95.14	073428	073428	073428	073428 human immunoglobulin heavy chain 1
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### ALIGNMENTS

RESULT	SEQUENCE	96 AA	11184 MW:	876DAB149144E286 CRC64;
1	073399	073399	073399	073399 human immunoglobulin heavy chain 1
2	073401	073401	073401	073401 human immunoglobulin heavy chain 1
3	073401	073401	073401	073401 human immunoglobulin heavy chain 1
4	073405	073405	073405	073405 human immunoglobulin heavy chain 1
5	073405	073405	073405	073405 human immunoglobulin heavy chain 1
6	073408	073408	073408	073408 human immunoglobulin heavy chain 1
7	073410	073410	073410	073410 human immunoglobulin heavy chain 1
8	073417	073417	073417	073417 human immunoglobulin heavy chain 1
9	073424	073424	073424	073424 human immunoglobulin heavy chain 1
10	073424	073424	073424	073424 human immunoglobulin heavy chain 1
11	073424	073424	073424	073424 human immunoglobulin heavy chain 1
12	073420	073420	073420	073420 human immunoglobulin heavy chain 1
13	073429	073429	073429	073429 human immunoglobulin heavy chain 1
14	073429	073429	073429	073429 human immunoglobulin heavy chain 1
15	073425	073425	073425	073425 human immunoglobulin heavy chain 1
16	073425	073425	073425	073425 human immunoglobulin heavy chain 1
17	073425	073425	073425	073425 human immunoglobulin heavy chain 1
18	073425	073425	073425	073425 human immunoglobulin heavy chain 1
19	073426	073426	073426	073426 human immunoglobulin heavy chain 1
20	073428	073428	073428	073428 human immunoglobulin heavy chain 1
21	073425	073425	073425	073425 human immunoglobulin heavy chain 1
22	073425	073425	073425	073425 human immunoglobulin heavy chain 1
23	073425	073425	073425	073425 human immunoglobulin heavy chain 1
24	073425	073425	073425	073425 human immunoglobulin heavy chain 1
25	073425	073425	073425	073425 human immunoglobulin heavy chain 1
26	073425	073425	073425	073425 human immunoglobulin heavy chain 1
27	073425	073425	073425	073425 human immunoglobulin heavy chain 1
28	073425	073425	073425	073425 human immunoglobulin heavy chain 1
29	073425	073425	073425	073425 human immunoglobulin heavy chain 1
30	073425	073425	073425	073425 human immunoglobulin heavy chain 1
31	073425	073425	073425	073425 human immunoglobulin heavy chain 1
32	073425	073425	073425	073425 human immunoglobulin heavy chain 1
33	073425	073425	073425	073425 human immunoglobulin heavy chain 1
34	073425	073425	073425	073425 human immunoglobulin heavy chain 1
35	073425	073425	073425	073425 human immunoglobulin heavy chain 1
36	073425	073425	073425	073425 human immunoglobulin heavy chain 1
37	073425	073425	073425	073425 human immunoglobulin heavy chain 1
38	073425	073425	073425	073425 human immunoglobulin heavy chain 1
39	073425	073425	073425	073425 human immunoglobulin heavy chain 1
40	073425	073425	073425	073425 human immunoglobulin heavy chain 1
41	073425	073425	073425	073425 human immunoglobulin heavy chain 1
42	073425	073425	073425	073425 human immunoglobulin heavy chain 1
43	073425	073425	073425	073425 human immunoglobulin heavy chain 1
44	073425	073425	073425	073425 human immunoglobulin heavy chain 1
45	073425	073425	073425	073425 human immunoglobulin heavy chain 1

DN	PARTIAL PROTEIN VIRUS GENE (IMI_MNT_ISOLATE) (FRAGMENT).	OC	Viruses; Retroviroidae; Lentiviruses.
VIR.		OX	NCBI_TaxID:11676;
ORG	Human immunodeficiency virus type 1.	RN	111
NAME		RA	SEGNI, Irakli N.A.
ID		RC	STRA_N-89_67
DEF	SEGNI, Irakli N.A.	RX	MEDLINE:9515640f; PubMed:783514;
AC	STRAIN IMI_MNT	RA	Kim P.M., Kolson D.L., Ballivet J.W., Srinivasan A., Collman R.G.;
BB	Marwa retroviruses protein comparison to Parted Pathogen F., Boussin F., RA	RT	"V3-independent determinants of macrophage tropism in a primary human
BT	Submitted (IMI_MNT_ISOLATE) to the IMB, 2004-07-14; last update, 2004-07-14; J. Virology, 69:1755-1761(1995).	RE	immunodeficiency virus type 1 isolate."
DR	EMBL: Z04204; GENBANK: U00242; PROTEIN: P00444; BLASTP: 1.0e-122.	RU	KL
DEF	Intervening sequence.	RE	J. Virology, 69:1755-1761(1995).
IDB	PROT522; VPR; 1.	RP	rti_21
DR	PROT522; VPR; 1.	RC	SEQUENCE FROM N.A.
DEF	SEGNI, Irakli N.A.; 11316 MW; DAE5365-AAPPEVF-CRGR4;	RA	STRA_N-89_67;
SEQ	09 ALTRIQLQPLHFRGCRHSRIGI 84	RX	MEDLINE:93059708; PubMed:1433527;
RESULT	4	RA	Collman R., Ballivet J.W., Gregory S.A., Friedman H., Kolson D.L.,
ID	07 3405	RT	"An infectious molecular clone of an unusual macrophage-tropic and
AC	07 3405	RE	lipolytic cytolytic strain of human immunodeficiency virus type 1;"
DR	01 AUG 1998 (EMBL:U00242; 07, created)	RL	J. Virology, 69:1755-1761(1995).
DR	01 OCT 2000 (EMBL:U00242; 07, last sequence update)	DR	EMBL: U03362; AAAA1039; 1;
DR	PARTIAL PROTEIN VIRUS GENE (IMI_MNT_ISOLATE) (FRAGMENT).	DR	TRANSAC: T02399; -;
GN	VIR.	DR	INTERPRO: IPR000112; -;
IS	Human immunodeficiency virus type 1.	DR	PROT522; VPR; 1.
VIRUSES	Retroviral viruses; Retroviridae; lentivirus.	SQ	PROTEINS: PROG44; BLVVPKX;
MTD	11676;	SEQUENCE	96 AA; 11316 MW; 213801934PMF248 CRC64;
BN		RESULT	5
RT	SEGNI, Irakli N.A.	Q9E248	Query Match
PA	Narwa retrovirus; Retropathogen; Parted Pathogen F., Boussin F.,	09E248	100.0%; Score 26; DB 14; length 96;
DR	Marwa retroviruses; Gag; hemagglutinin; gp120; gp41; Env; gp140; DR	PRELIMINARY:	Best local Similarity 100.0%; Pred. No. 2.4e-19; Mismatches 0; Indexes 0; Gaps 0;
DR	01 AUG 1998 (EMBL:U00242; 07, last sequence update)	RT	5.9 ALTRIQLQPLHFRGCRHSRIGI 84
DR	PARTIAL PROTEIN VIRUS GENE (IMI_MNT_ISOLATE) (FRAGMENT).	ID	Q9E248
GN	VIR.	AC	Q9E248;
IS	Human immunodeficiency virus type 1.	ID	Q9E248;
VIRUSES	Retroviral viruses; Retroviridae; lentivirus.	BT	01-MAR-2001 (EMBL:U00242; 07, created)
MTD	11676;	ID	01-MAR-2001 (EMBL:U00242; 07, last sequence update)
BN		DE	01-MAR-2001 (EMBL:U00242; 07, last sequence update)
RT	SEGNI, Irakli N.A.	GN	VPR PROTEIN (FRAGMENT).
PA	Alfred N. Yedavalli V.S.R.K.;	AC	Q9E248
DR	"Low conservation of Functional Domains of Human Immunodeficiency	ID	Q9E248
DR	Virus Type 1 virus and vpr genes correlates with lack of vertical	BT	Transmission;"
DR	Transmission;"	ID	Q9E248
DR	Segni, Irakli N.A.; 11316 MW; 213801934PMF248 CRC64;	RE	Q9E248; AL02275139; AAC23277_1; -;
DR	Q9E248; AL02275139; AAC23277_1; -;	RC	Q9E247
DEF	Human immunodeficiency virus type 1.	RE	Q9E247
IDB		RC	Q9E247
DR		RA	Q9E247
DEF		RT	Q9E247
SEQ	09 ALTRIQLQPLHFRGCRHSRIGI 84	RC	Q9E247
RESULT	4	RC	Q9E247
ID	07 3409	RA	Q9E247
AC	07 3409	RT	Q9E247
BT	01 NOV 1996 (EMBL:U00242; 07, created)	RE	Q9E247
ID	01 NOV 1996 (EMBL:U00242; 07, last sequence update)	RC	Q9E247
DR	01 MAY 2010 (EMBL:U00242; 07, last annotation update)	RN	Q9E247
DR	VPR PROTEIN.	RN	Q9E247
GN	VPR	RA	Q9E247
IS	Human immunodeficiency virus type 1.	RT	Q9E247





Query Match	95.28%	Score	25	DB	14	length	94																																				
host torai Similarity	100.0%	Prod.	No.	2	4x-18																																						
Matches	25	Conservative	3	Nimatches	0	Indices	0																																				
Y	1	A	L	R	I	Q	U	J	F	H	R	I	S	T	R	I	S	I	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25
Y	59	A	L	K	Q	M	I	H	R	G	C	R	S	I	G	I	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25		

RESULT 15  
071918  
ID 071918 PRELIMINARY PRT; 95 AA.  
AT 071918;  
DT 01-MAY-1996 (TREMBL1, 01, last sequence update)  
DT 01-MAY-2000 (TREMBL1, 13, Last annotation update)  
DR CTRIC\_1, CLONE\_4, ACCESSORY REGION GENES, COMPLETE CDS,  
PR VPR.  
OS Human immunodeficiency virus type 1.  
OC Human immunodeficiency virus type 1.  
OC Retroviridae: proviridae; Lentivirus.

SEQUENCE OF 1-20 FROM N.A.  
STRAIN-CTRL TISSUE-BLK

MEIDLINE-95287475; PubMed-777

Michael N.L., Chang G.Y., Arcey L.M.,  
Busch M.P., Wier D.L., Schwartz D.J.  
Bischoff, progressive disease in a child  
infected from birth. *J Infect Dis* 1991;

J. VICKI L. 69:4 228-236 (1995)

SEQUENCE FROM N.A.  
STRAIN CNI:K1; TISSUE: Bladder

A  
Michael N. L.;  
Submitted (APP-1495) to the  
FEDERAL TRADE COMMISSION

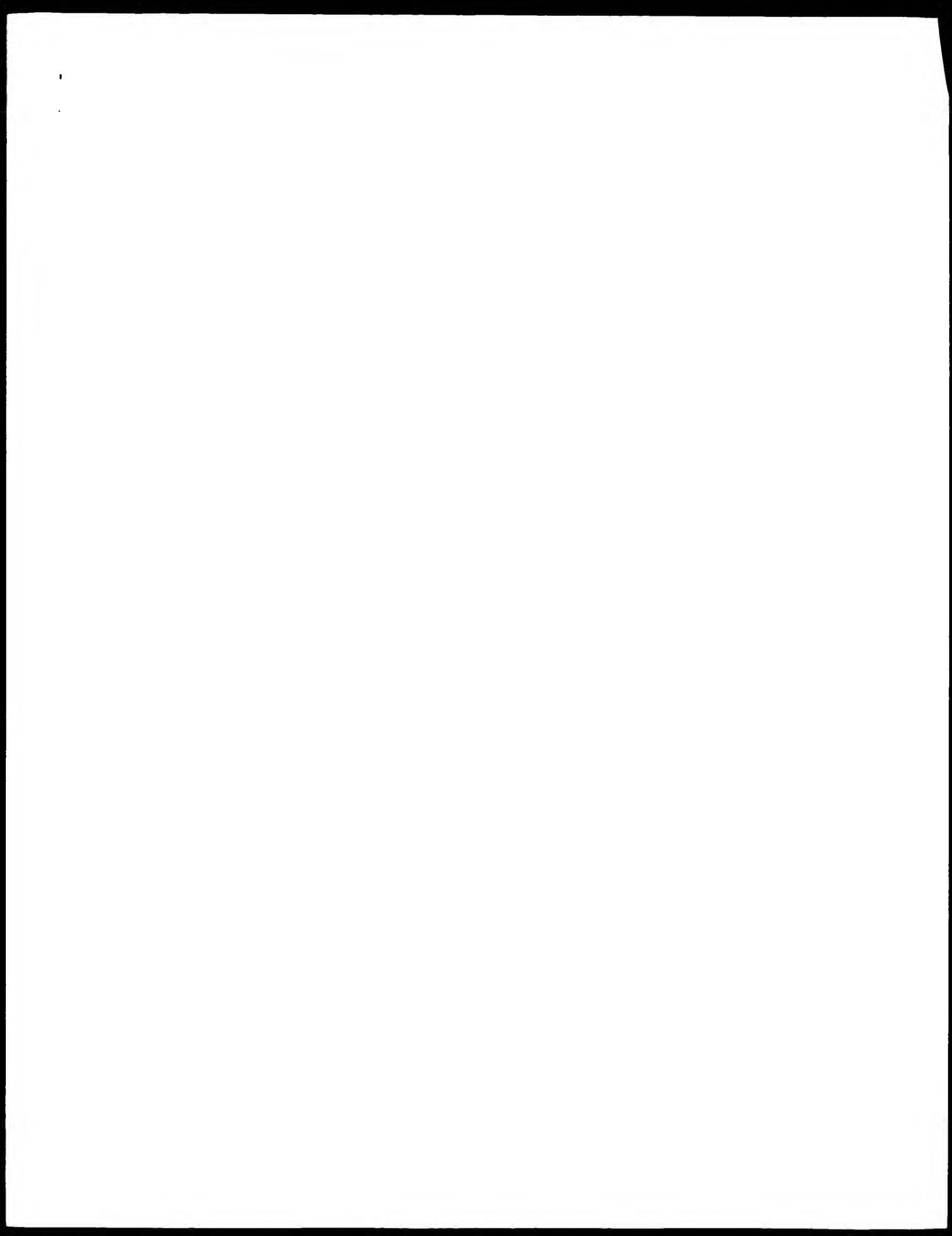
EMBL; 024436; RAY 9508.1; -  
InterPro; IPR000012; -  
Pfam; PF00522; VPR; 1;

PRINIS; PKD0444; HIWVPRV<sup>P</sup>X;  
SEQUENCE: 95 AA; 11251 MW

Query	Match	Similarity	96.2%
Best local similarity	100.0%		

WY  
1 ALIRISQALAFIHRIGCRHSRIGI 25  
MARCHES 26. 1880. M.

59 ALKALOID IN THE CRASSIFOLIA



Sequence: 1 ALIRIQLQILFTHFRIGCRHSRIGLII 26									
Scoring table: OLS05									
Word size : 0									
Searched: 93435 seqs, 34255486 residues									
Total number of hits satisfying chosen parameters: 93435									
Minimum DB seq length: 0									
Maximum DB seq length: 26000000									
Post-processing: visiting first 45 summaries									
Database : SwissProt_39,*									
pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.									
SUMMARIES									
Result No.	Score	Query	Length	DB ID	Description	RESULT	STANDARD	PRT	96 AA.
1	24	92.3	96	1 VPR_HV1MN	P02950 human immunodeficiency virus type 1 (MR isolate) (HIV-1).	10 VPR_HV1MN	STANDARD	PRT	96 AA.
2	24	92.3	96	1 VPR_HV1SC	Guapo C., Guo H.-G., Franchini G., Aldovini A., Collatti E.,	10 VPR_HV1MN	STANDARD	PRT	96 AA.
3	23	92.3	96	1 VPR_HV1TP	Fairall R., Wang Siaai L., Gallo R., Kottitz M.S. Jr.,	10 VPR_HV1MN	STANDARD	PRT	96 AA.
4	22	94.6	96	1 VPR_HV1PR	"Envelope" sequences of two new United States HIV-1 isolates.";	10 VPR_HV1MN	STANDARD	PRT	96 AA.
5	22	94.6	96	1 VPR_HV1NC	Virology 164:541-556 (1988).	10 VPR_HV1MN	STANDARD	PRT	96 AA.
6	22	94.6	96	1 VPR_HV1DZ	--	10 VPR_HV1MN	STANDARD	PRT	96 AA.
7	16	61.5	96	1 VPR_HV1OY	MISCELLANEOUS: THE MN ISOLATE WAS TAKEN FROM A PATIENT IN 1984.	10 VPR_HV1MN	STANDARD	PRT	96 AA.
8	16	61.5	96	1 VPR_HV1RH	CC This SWISS-PROT entry is copy-right. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non profit institutions as long as its content is in no way modified and this statement is mentioned. "copy-right by and for commercial entities requires a license agreement (see http://www.ebi.ac.uk/~mccoll/). Or send an email to license@ebi.soton.ac.uk".	10 VPR_HV1MN	STANDARD	PRT	96 AA.
9	16	61.5	97	1 VPR_HV1A2	DR FMBU: M17449; VIRSMN:	10 VPR_HV1MN	STANDARD	PRT	96 AA.
10	16	61.5	97	1 VPR_HV1C	DR Interpro: IPI000012; --;	10 VPR_HV1MN	STANDARD	PRT	96 AA.
11	16	61.5	97	1 VPR_HV1D	DE FIBM: M17452; VFE: 1.	10 VPR_HV1MN	STANDARD	PRT	96 AA.
12	13	50.0	96	1 VPR_HV1B1	DP PPTINS: PR00444; HTWPPVX.	10 VPR_HV1MN	STANDARD	PRT	96 AA.
13	12	46.2	78	1 VPR_HV1B2	RW AIDS: 1134 MW.	10 VPR_HV1MN	STANDARD	PRT	96 AA.
14	12	46.2	99	1 VPR_HV1B5	SEQUENCE: 96 AA. 1134 MW. 295P12E25755CE 3064;	10 VPR_HV1MN	STANDARD	PRT	96 AA.
15	8	30.8	101	1 VPR_HV1SP	PR0287 chimpanzee	10 VPR_HV1MN	STANDARD	PRT	96 AA.
16	7	26.9	96	1 VPR_HV1C2	PR0284 simian 2	10 VPR_HV1MN	STANDARD	PRT	96 AA.
17	7	26.9	451	1 VPR_HV1CA	PR0284 simian 2	10 VPR_HV1MN	STANDARD	PRT	96 AA.
18	6	23.1	89	1 VPR_HV1CA	PR0285 simian 2	10 VPR_HV1MN	STANDARD	PRT	96 AA.
19	6	23.1	87	1 VPR_HV1MR	PR0286 simian 2	10 VPR_HV1MN	STANDARD	PRT	96 AA.
20	6	23.1	101	1 VPR_HV1MI	PR0287 human immunodeficiency virus type 1 (MR isolate) (HIV-1).	10 VPR_HV1MN	STANDARD	PRT	96 AA.
21	6	23.1	101	1 VPR_HV1ST	PR02884 human immunodeficiency virus type 1 (MR isolate) (HIV-1).	10 VPR_HV1MN	STANDARD	PRT	96 AA.
22	6	23.1	105	1 VPR_HV1TC	PR02896 human immunodeficiency virus type 1 (MR isolate) (HIV-1).	10 VPR_HV1MN	STANDARD	PRT	96 AA.
23	6	23.1	105	1 VPR_HV1W	PR02897 human immunodeficiency virus type 1 (MR isolate) (HIV-1).	10 VPR_HV1MN	STANDARD	PRT	96 AA.
24	6	23.1	122	1 VPR_HV1ML	PR028755 mycobacterium	10 VPR_HV1MN	STANDARD	PRT	96 AA.
25	6	23.1	123	1 VPR_HV1MCM	PR028761 escherichia	10 VPR_HV1MN	STANDARD	PRT	96 AA.
26	6	23.1	219	1 VPR_HV1MGT	PR028773 saccharomyces	10 VPR_HV1MN	STANDARD	PRT	96 AA.
27	6	23.1	242	1 VPR_HV1YAT	PR028773 bacterium	10 VPR_HV1MN	STANDARD	PRT	96 AA.
28	6	23.1	253	1 VPR_HV1BAC	PR028773 bacterium	10 VPR_HV1MN	STANDARD	PRT	96 AA.
29	6	23.1	353	1 VPR_HV1MONSE	PR028484 mouse	10 VPR_HV1MN	STANDARD	PRT	96 AA.
30	6	23.1	379	1 VPR_HV1CAB	PR0287735 campylobacter	10 VPR_HV1MN	STANDARD	PRT	96 AA.
31	6	23.1	380	1 VPR_HV1KFC	PR0287736 mycobacterium	10 VPR_HV1MN	STANDARD	PRT	96 AA.
32	6	23.1	394	1 VPR_HV1PAT	PR0287737 rat/mouse	10 VPR_HV1MN	STANDARD	PRT	96 AA.
33	6	23.1	394	1 VPR_HV1PAT	PR0287738 homo sapien	10 VPR_HV1MN	STANDARD	PRT	96 AA.
34	6	23.1	394	1 VPR_HV1PAT	PR0287739 caenorhabditis elegans	10 VPR_HV1MN	STANDARD	PRT	96 AA.
35	6	23.1	394	1 VPR_HV1PAT	PR0287740 saccharomyces cerevisiae	10 VPR_HV1MN	STANDARD	PRT	96 AA.
36	6	23.1	394	1 VPR_HV1PAT	PR0287741 amniota	10 VPR_HV1MN	STANDARD	PRT	96 AA.
37	6	23.1	394	1 VPR_HV1PAT	PR0287742 orctolaeus	10 VPR_HV1MN	STANDARD	PRT	96 AA.
38	6	23.1	394	1 VPR_HV1PAT	PR0287743 rattus norvegicus	10 VPR_HV1MN	STANDARD	PRT	96 AA.
39	6	23.1	394	1 VPR_HV1PAT	PR0287744 mus musculus	10 VPR_HV1MN	STANDARD	PRT	96 AA.
40	6	23.1	394	1 VPR_HV1PAT	PR0287745 apomys humeralis	10 VPR_HV1MN	STANDARD	PRT	96 AA.
41	6	23.1	394	1 VPR_HV1PAT	PR0287746 opossum	10 VPR_HV1MN	STANDARD	PRT	96 AA.
42	6	23.1	394	1 VPR_HV1PAT	PR0287747 tarsius spectrum	10 VPR_HV1MN	STANDARD	PRT	96 AA.
43	6	23.1	394	1 VPR_HV1PAT	PR0287748 cercopithecus aethiops	10 VPR_HV1MN	STANDARD	PRT	96 AA.
44	6	23.1	394	1 VPR_HV1PAT	PR0287749 cercopithecus abyssinicus	10 VPR_HV1MN	STANDARD	PRT	96 AA.
45	6	23.1	394	1 VPR_HV1PAT	PR0287750 cercopithecus nigeryanus	10 VPR_HV1MN	STANDARD	PRT	96 AA.



OS Human immunodeficiency virus type 1 (New York-5 isolate) (HIV-1).  
 OC Viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxId:11698;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA buckler c.f., buckler-white a.j., willley k.l., mccoy j.j.  
 RL Submitted by CIRI Team to the EMBL protein databases.  
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 DR EMBL: M13921; AAAA4690; 1;  
 DR HIV; M13921; VPRS13; 1;  
 DR InterPro: IPR00522; 1;  
 DR PRTM: PRO00522; VPR; 1;  
 DR PRTM: PRO0044; HIVVPPVX  
 KW AIDS; SEQUENCE  
 SQ >6 AA. 11579 MW. 56855<73473450>R264;

Query Match Similarity 84.6%; Score 227; DB 1; Length 96;  
 Best Local Similarity 100.0%; Pred. No. 1; ac-16;  
 AC ID 01-MAR-1998 (Rel. 09, created)  
 DT 01-MAR-1998 (Rel. 09, last sequence update)  
 DT 01-JUL-1993 (Rel. 26, last annotation update)  
 CC VIP PROTEIN (R ORF PROTEIN).  
 CC VIR.  
 CC HIV-1, human immunodeficiency virus type 1 (New York-5 isolate) (HIV-1).  
 CC Viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID:11698;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 DR SHUJIN M., WAIHOLATION S., MENAQUER L., SONIJO P.;  
 DR "Genetic variability of the AIDS virus: nucleotide sequence analysis  
 of two isolates from African patients.";  
 DR Cell 46:383-391(1986).  
 CC  
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 CC  
 DR EMBL: K03454; AAAA4327; 1;  
 DR InterPro: IPR00522; VPR; 1;  
 DR PRTM: PRO00522; VPR; 1;  
 DR HIV; K03454; VPRSM1;  
 DR InterPro: IPR00522; VPR; 1;  
 DR PRTM: PRO0044; HIVVPPVX.  
 KW AIDS; SEQUENCE  
 SQ >6 AA. 11305 MW. F47E52F1292741>R254;

Query Match Similarity 61.5%; Score 16; DB 1; Length 96;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+10;  
 Matches 16; Consistency 5; MisMatches 9; Index 9; Gaps 0;  
 AC P20591;  
 DT 01-FEB-1991 (Rel. 17, created)  
 DT 01-FEB-1991 (Rel. 17, last sequence update)  
 DT 01-JUL-1993 (Rel. 26, last annotation update)  
 DE VPR PROTEIN (R ORF PROTEIN).  
 GN VPR.  
 OC Human immunodeficiency virus type 1 (NY isolate) (HIV-1).  
 OC Viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID:11683;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Theodore J., Buckler-White A.;  
 RL Submitted (NOV 1983) to the HIV data bank.  
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 DR EMBL: M22649; AAAA5368; 1;  
 DR HIV; M22649; VPRS13; 1;  
 DR InterPro: IPR00522; VPR; 1;  
 DR PRTM: PRO00522; VPR; 1;  
 DR PRTM: PRO0044; HIVVPPVX.  
 KW AIDS; SEQUENCE  
 SQ >6 AA. 11380 MW. 85B24A10559A944>R254;

Query Match Similarity 69.2%; Score 19; DB 1; Length 96;  
 Best Local Similarity 100.0%; Pred. No. 2e+12;  
 Matches 19; Consistency 6; MisMatches 6; Index 6; Gaps 0;  
 AC  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE 90148544; Pubmed-255979;  
 RA Huet T., Datta M.C., Brun-Vezinet F., Koelants G.E., Wain-Hobson S.,  
 RL "A highly defective HIV-1 strain isolated from a healthy Gabonese  
 individual presenting an atypical western blot";  
 RL AIDS 3:707-715(1989);  
 OC -- MISCELLANEOUS: The oxy isolate was TAKEN FROM THE BLOOD OF A  
 CC HEALTHY GABONSE INDIVIDUAL.



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 CC  
 DR EMBL: M3358; -; NOT\_ANNOTATED\_CDS.  
 DR PIR: D44001; 644603;  
 DR INTERPRO: IPR00012;  
 DR BREN: IPR0002; VPF: 1;  
 DR PRINTS: PRO044; BLWVPRPX.  
 KW AIDS;  
 KW Shenoy, G. A.; 11475 MW; CPTC4834F6A497 CP64;  
 KW  
 KW  
 RESULT 12  
 VPR\_HV1MA  
 ID VPR\_HV1MA STANDARD; PRT; 96 AA.  
 AC P05457;  
 DT 01-NOV-1998 (rel. no. Created)  
 DT 01-NOV-1998 (rel. no. Last sequence update)  
 DT 01-JUL-1993 (rel. 26, Last annotation update)  
 DE VPR\_HV1MA (see VPR\_HV1R).  
 GN VPR.  
 OS Human immunodeficiency virus type 1 (MA1 isolate) (HIV-1)  
 OC Viruses; Retrovirus viruses; retroviridae; sequence analysis  
 OC NCBI\_TAXID:11697;  
 RN 111  
 RP SEQUENCE FROM N.A.  
 RP  
 RN SEQUENCE FROM N.A.  
 RP STRAIN ISOLATE BX10;  
 RP MEDLINE:8511237; PubMed=30466;  
 RA Rattner L., Fischer A., Jezdecinski L.I., Mitsuya H., Lion R.-S.,  
 PA Rosenthal S.P., Borczyk E.R., Ratalski T.A., Whitham R.A.,  
 RA Gamreitzer K., Bryant T., Potokay S.B., Jr., Pearson M.L., Gallo R.C.,  
 RA Lautenberger J.A., Papas T.S., Ghayyat J., Chang N.I., Gallo R.C.,  
 RA Wenz-Saal P.;  
 RT "Complete nucleotide sequence of the AIDS virus, HTLV-III.";  
 RL Nature 313:277-284(1985);  
 RL [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN ISOLATE BXB2;  
 RC MEDLINE:8522849; PubMed=308154;  
 RA Rattner L., Fischer A., Jezdecinski L.I., Mitsuya H., Lion R.-S.,  
 RA Gallo R.C., Wenz-Saal P.;  
 RT "Complete nucleotide sequences of functional clones of the AIDS  
 virus.";  
 RL AIDS Res. Hum. Retroviruses 3:57-69(1987);  
 RL [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN ISOLATE BXB3;  
 RC MEDLINE:8522849; PubMed=2998795;  
 RA Gross F., Samotaj S.J., Sojda M., Zentz V., Reiss J., Schatzl M., Kramer E.,  
 RA Shaw G.M., Wenz-Saal P., Reddy E.P.;  
 RA HIV-111 clade products synthesized in E. coli are recognized by  
 RA antibodies present in the sera of AIDS patients.";  
 RL (cell 41:179-98(1985)).  
 RL [4]  
 RT SEQUENCE FROM N.A.  
 RA MEDLINE:8522849; PubMed=308154;  
 RA Arya S.K., Gallo R.C.;  
 RT "Three novel genetic human T-lymphotropic virus type III: immune  
 reactivities of the products with sera from acquired immune  
 deficiency syndrome patients.";  
 RT "Antigenic specificity of products with sera from acquired immune  
 deficiency syndrome patients.";  
 PR Price N.M.; Acydi S.; Schatzl M.;  
 RN 151  
 RP SEQUENCE FROM N.A.  
 RC STRAIN ISOLATE PV22;  
 RC MEDLINE:8511157; PubMed=2982104;  
 RA Mascher M.A., Smith D.H., Catrullina O.L., Paxton G.V., Lasky L.A.,  
 RA Capon D.J.;  
 RT "Nucleic acid structure and expression of the human  
 AIDS/HIV-1 provirus.";  
 RT AIDS/HIV-1 provirus.";  
 RL Matzke S.I.; 153:175-178(1985).  
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 DR EMBL: K02893; AAA44203\_1;  
 DR EMBL: X01762; NOT\_ANNOTATED\_CDS.  
 DR EMBL: K03455; AAA4961\_1;  
 DR EMBL: M11040; AAA4998\_1;  
 DR EMBL: M14100; AAA4975\_1;  
 DR  
 HIV; M15654; VPRSH102.

RESULT 13  
 VIR\_HV1B1  
 ID VIR\_HV1B1 STANDARD; PRT; 78 AA.  
 AC P05457; Q85577;  
 DT 01-NOV-1998 (rel. 06, Created)

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FBI-BIRMINGHAM

Macchesi 12; Nascimbene 10; Misnashayev 11; Tardieu 12; Gori 13; Siviero 13; Vassalli 14; Siviero 19; 14, 15; Riva 16; Nature 345: 646-649 (1990).

**REVIEW** **A**  
**VIP LIV Bc**

"Molecular clones from a non-acutely pathogenic derivative of SV40/MB4: characterization and comparison to acutely pathogenic clones." *J Virol* 1990; 64: 103-110.

REVIEWED BY A. A. RUSSELL HORN, RECOMMENDED FOR THE SWISS STANDARD OF PRACTICE IN THE FIELD OF DENTAL EDUCATION

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EMBL: 103495; RAB5/77317;  
EMBL: 103298; AAAA477801;

RE: Nature 313:277-284 (1994).  
Sequence of the AIDS virus HIV 111.

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on 00 stored an email for [frank@psb.silv.ch](mailto:frank@psb.silv.ch)

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Match time: 286 sec

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